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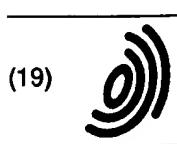
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(54) NOVEL PROTEIN AND METHODS FOR THE PRODUCTION OF THE SAME

(57) A protein which inhibits osteoclast differentiation and/or maturation and a method of production of the protein. The protein is produced by human embryonic lung fibroblasts and has molecular weight of about 60 kD and about 120 kD under non-reducing conditions and about 60 kD under reducing conditions on SDS-polyacrylamide gel electrophoresis, respectively.

The protein can be isolated and purified from culture medium of the said fibroblasts. Furthermore, the protein can be produced by gene engineering.

The present invention includes cDNA for producing the protein by gene engineering, antibodies having specific affinity to the protein or a method for determination of the protein concentration using the antibodies.

Description**Field of the invention**

5 This invention relates to a novel protein, osteoclastogenesis inhibitory factor (OCIF), and methods for producing the protein.

Background of the invention

10 Human bones are always remodelling by the repeated process of resorption and reconstitution. In the process, osteoblasts and osteoclasts are considered to be the cells mainly responsible for bone formation and bone resorption, respectively. A typical example of disease caused by the progression of abnormal bone metabolism is osteoporosis. The disease is known to be provoked by the condition in which bone resorption by osteoclasts exceeds bone formation by osteoblasts, but the mechanism of osteoporosis has not yet been completely elucidated. Osteoporosis causes pain 15 in the bone and makes the bone fragile, leading to fracture. Since osteoporosis increases the number of bedridden old people, it has become a social issue with the increasing number of old people. Therefore, efficacious drugs for the treatment of the disease are expected to be developed. Bone mass reduction caused by the abnormal bone metabolism is thought to be prevented by inhibiting bone resorption, improving bone formation, or improving the balanced metabolism.

20 Bone formation is expected to be promoted by stimulating growth, differentiation, or activation of osteoblasts. Many cytokines are reported to stimulate growth or differentiation of osteoblasts, i.e. fibroblast growth factor (FGF) (Rodan S. B. et al., Endocrinology vol. 121, p1917, 1987), insulin-like growth factor-I (IGF-I) (Hock J.M. et al., Endocrinology vol. 122, p254, 1988), insulin-like growth factor-II (IGF-II) (McCarthy T. et al., Endocrinology vol. 124, p301, 1989), Activin A (Centrella M. et al., Mol. Cell. Biol. vol. 11, p250, 1991), Vasculotropin (Varonique M et al., Biochem. Biophys. Res. Commun. vol. 199, p380, 1994), and bone morphogenetic protein (BMP) (Yamaguchi, A et al., J. Cell Biol. vol. 113, p682, 1991, Sampath T.K. et al., J. Biol Chem. vol. 267, p20532, 1992, and Knutson R. et al., Biochem. Biophys. Res. Commun. vol. 194, p1352, 1993).

25 On the other hand, cytokines which inhibits differentiation and/or maturation of osteoclasts have been paid attention and have been intensively studied. Transforming growth factor- β (Chen C. et al., Proc. Natl. Acad. Sci. USA, vol. 85, p5683, 1988) and interleukin-4 (Kasano K. et al., Bone-Miner., vol. 21, p179, 1993) are found to inhibit the differentiation of osteoclasts. Calcitonin (Bone-Miner., vol. 17, p347, 1992), Macrophage colony-stimulating factor (Hattersley G. et al. J. Cell. Physiol. vol. 137, p199, 1988), interleukin-4 (Watanabe, K. et al., Biochem. Biophys. Res. Commun. vol. 172, p1035, 1990), and interferon- γ (Gowen M. et al., J. Bone Miner. Res., vol. 1, p469, 1986) are found to inhibit bone resorption by osteoclasts.

30 These cytokines are expected to be efficacious drugs for improving bone mass reduction by stimulating bone formation and/or by inhibiting bone resorption. The cytokines such as insulin like growth factor-I and bone morphogenetic proteins are now investigated in clinical trials for their effects in treatment of patients with bone diseases. Calcitonin is already used as a drug to care osteoporosis and to diminish pain in osteoporosis.

35 Examples of drugs now clinically utilized for the treatment of bone diseases and for shortening the treatment period are dihydroxyvitamine D₃, vitamin K₂, calcitonin and its derivatives, hormones such as estradiol, ipriflavon, and calcium preparations. However, these drugs do not provide satisfactory therapeutic effects, and novel drug substances have been expected to be developed. As mentioned, bone metabolism is controlled in the balance between bone resorption and bone formation. Therefore, cytokines which inhibit osteoclast differentiation and/or maturation are expected to be developed as drugs for the treatment of bone diseases such as osteoporosis.

45 Disclosure of Invention

This invention was initiated from the view point described above. The purpose of this invention is to offer both a novel factor termed osteoclastogenesis inhibitory factor (OCIF) and a procedure to produce the factor efficiently.

50 The inventors have intensively searched for osteoclastogenesis inhibitory factors in human embryonic fibroblast IMR-90 (ATCC CCL186) conditioned medium and have found a novel osteoclastogenesis inhibitory factor (OCIF) which inhibits differentiation and/or maturation of osteoclasts.

The inventors have established a method for accumulating the protein to a high concentration by culturing IMR-90 cells using alumina ceramic pieces as the cell adherence matrices.

55 The inventors have also established an efficient method for isolating the protein, OCIF, from the IMR-90 conditioned medium using the following sequential column chromatography, ion-exchange, heparin affinity, cibacron-blue affinity, and reverse phase.

The inventors, based on the amino acid sequence of the purified natural OCIF, successfully cloned a cDNA encod-

ing this protein. The inventors established also a procedure to produce this protein which inhibits differentiation of osteoclasts. This invention concerns a protein which is produced by human lung fibroblast cells, has molecular weights in SDS-PAGE of 60 KD in the reducing conditions and 120 KD under the non-reducing conditions, has affinity for both cation-exchange resins and heparin, reduces its activity to inhibit differentiation and maturation of osteoclasts if treated for 5 10 minutes at 70 °C or for 30 minutes at 56 °C, and lose its activity to inhibit differentiation and maturation of osteoclasts by the treatment for 10 minutes at 90 °C. The amino acid sequence of the protein OCIF which is described in the present invention is clearly different from any of known factors inhibiting formation of osteoclasts.

The invention includes a method to purify OCIF protein, comprising : (1) culturing human fibroblasts, (2) applying the conditioned medium to a heparin column to obtain the adsorbed fraction, (3) purifying the OCIF protein using a cation-exchange column, (4) purifying the OCIF protein using a heparin affinity column, (5) purifying the OCIF protein using a cibacron blue affinity column, (6) isolating the OCIF protein using reverse-phase column chromatography. Cibacron blue F3GA coupled to a carrier made of synthetic hydrophilic polymers is an example of materials used to prepare Cibacron blue columns. These columns are conventionally called "blue columns".

10 The invention includes a method for accumulating the OCIF protein to a high concentration by culturing human fibroblasts using alumina ceramic pieces as the cell-adherence matrices.

15 Moreover, the inventors determined the amino acid sequences of the peptides derived from OCIF, designed the primers based on these amino acid sequences, and obtained cDNA fragments encoding OCIF from a cDNA library of IMR-90 cells.

20 Detailed description of the invention

The OCIF protein of the present invention can be isolated from human fibroblast conditioned medium with high yield. The procedure to isolate OCIF is based on ordinary techniques for purifying proteins from biomaterials, in accordance with the physical and chemical properties of OCIF protein. For example, concentrating procedure includes ordinary biochemical techniques such as ultrafiltration, lyophilization, and dialysis. Purifying procedure includes combinations of several chromatographic techniques for purifying proteins such as ion-exchange column chromatography, affinity column chromatography, gel filtration column chromatography, hydrophobic column chromatography, reverse phase column chromatography, and preparative gel electrophoresis. The human fibroblast used for production of the OCIF protein is preferably IMR-90. A method for producing the IMR-90 conditioned medium is preferably a process comprising, adhering human embryonic fibroblast IMR-90 cells to alumina ceramic pieces in roller-bottles, using DMEM medium supplemented with 5 % new born calf serum for the cell culture, and cultivating the cells in roller-bottles for 7 to 10 days by stand cultivation. CHAPS (3-[(3-cholamidopropyl)-dimethylammonio]-1-propanesulfonate) is preferably added to the buffer as a detergent in the purification steps of OCIF protein.

25 OCIF protein of the instant invention can be initially obtained as a heparin binding basic OCIF fraction by applying the culture medium to a heparin column (Heparin-Sepharose CL-6B, Pharmacia), eluting with 10 mM Tris-HCl buffer, pH 7.5, containing 2 M NaCl, and then by applying the OCIF fraction to a Q + anion-exchange column (HiLoad-Q/FF, Pharmacia), and collecting non-adsorbed fraction. OCIF protein can be purified by subjecting the obtained OCIF fraction to purification on a S + cation-exchange column (HiLoad-S/FF, Pharmacia), a heparin column (Heparin-5PW, TOSOH), Cibacron Blue column (Blue-5PW, TOSOH), and a reverse-phase column (BU-300 C4, Perkin Elmer) and 30 the material is defined by the previously described properties.

35 The present invention relates to a method of cloning cDNA encoding the OCIF protein based on the amino acid sequence of natural OCIF and a method of obtaining recombinant OCIF protein that inhibits differentiation and/or maturation of osteoclasts. The OCIF protein is purified according to the method described in the present invention and is treated with endopeptidase (for example, lysylendopeptidase). The amino acid sequences of the peptides produced by 40 the digestion are determined and the mixture of oligonucleotides that can encode each internal amino acid sequence was synthesized. The OCIF cDNA fragment is obtained by PCR (preferably RT-PCR, reverse transcriptase PCR) using the oligonucleotide mixtures described above as primers. The full length OCIF cDNA encoding the OCIF protein is cloned from a cDNA library using the obtained OCIF DNA fragment as a probe. The OCIF cDNA containing the entire coding region is inserted into an expression vector. The recombinant OCIF can be produced by expressing the OCIF 45 cDNA containing the entire coding region in mammalian cells or bacteria.

50 The present invention relates to the novel proteins OCIF2, OCIF3, OCIF4, and OCIF5 that are variants of OCIF and have the activity described above. These OCIF variants are obtained from the cDNA library constructed with IMR-90 poly(A) + RNA by hybridization using the OCIF cDNA fragment as a probe. Each of the OCIF variant cDNAs containing the entire coding region is inserted into an expression vector. Each recombinant OCIF variant can be produced by 55 expressing each of the OCIF variant cDNAs containing the entire coding region in the conventional hosts. Each recombinant OCIF variant can be purified according to the method described in this invention. Each recombinant OCIF variant has an ability to inhibit osteoclastogenesis.

The present invention further includes OCIF mutants. They are substitution mutants comprising replacement of one

cysteine residue possibly involved in dimer formation with serine residue, and various deletion mutants of OCIF. Substitutions or deletions are introduced into the OCIF cDNA using polymerase chain reaction (PCR) or by restriction enzyme digestion. Each of these mutated OCIF cDNAs is inserted into a vector containing an appropriate promoter for gene expression. The resultant expression vector for each of the OCIF mutants is transfected into eukaryotic cells such as mammalian cells. Each of OCIF mutants can be obtained and purified from the conditioned media of the transfected cells.

The present invention provides polyclonal antibodies and a method to quantitatively determine OCIF concentration using these polyclonal antibodies.

As antigens (immunogens), natural OCIF obtained from IMR-90 conditioned medium, recombinant OCIF produced by such hosts as microorganisms and eukaryotes using OCIF cDNA, synthetic peptides designed based on the amino acid sequence of OCIF, or peptides obtained from OCIF by partial digestion can be used. Anti-OCIF polyclonal antibodies are obtained by immunizing appropriate mammals with the antigens in combination with adjuvants for immunization if necessary, purifying from the serum by the ordinary purification methods. The anti-OCIF polyclonal antibodies which are labelled with radioisotopes or enzymes can be used in radio-immunoassay (RIA) system or immunoassay (EIA) system. By using these assay systems, the concentrations of OCIF in biological materials such as blood and ascites and cells-culture medium can be easily determined.

The antibodies in the present invention can be used in radio immunoassay (RIA) or enzyme immunoassay (EIA). By using these assay systems, the concentration of OCIF in biological materials such as blood and ascites can be easily determined.

The present invention provides novel monoclonal antibodies and a method to quantitatively determine OCIF concentration using these monoclonal antibodies.

Anti-OCIF monoclonal antibodies can be produced by the conventional method using OCIF as an antigen. Native OCIF obtained from the culture medium of IMR-90 cells and recombinant OCIF produced by such hosts as microorganisms and eukaryotes using OCIF cDNA can be used as antigens. Alternatively, synthesized peptides designed based on the amino acid sequence of OCIF and peptides obtained from OCIF by partial digestion can be also used as antigens. Immunized lymphocytes obtained by immunization of mammals with the antigen or by an in vitro immunization method were fused with myeloma of mammals to obtain hybridoma. The hybridoma clones secreting antibody which recognizes OCIF were selected from the hybridomas obtained by the cell fusion. The desired antibodies can be obtained by cell culture of the selected hybridoma clones. In preparation of hybridoma, small animals such as mice or rats are generally used for immunization. To immunize, OCIF is suitably diluted with a saline solution (0.15 M NaCl), and is intravenously or intraperitoneally administered with an adjuvant to animals for 2 -5 times every 2 -20 days. The immunized animal was killed three days after final immunization, the spleen was taken out and the splenocytes were used as immunized B lymphocytes.

Mouse myeloma cell lines for cell fusion with the immunized B lymphocytes include, for example, p3/x63-Ag8, p3-U1, NS-1, MPC-11, SP-2/0, FO, p3x63 Ag8.653, and S194. Rat R-210 cell line may also be used. Human B lymphocytes are immunized by an in vitro immunization method and are fused with human myeloma cell line or EB virus transformed human B lymphocytes which are used as a parent cell line for cell fusion, to produce human type antibody.

Cell fusion of the immunized B lymphocytes and myeloma cell line is carried out principally by the conventional methods. For example, the method of Koehler G. et al. (*Nature* **256**, 495-497, 1975) is generally used, and also an electric pulse method can be applied to cell fusion. The immunized B lymphocytes and transformed B cells are mixed at conventional ratios and a cell culture medium without FBS containing polyethylene glycol is generally used for cell fusion. The B lymphocytes fused with myeloma cell lines are cultured in HAT selection medium containing FBS to select hybridoma.

For screening of hybridoma producing anti-OCIF antibody, EIA, plaque assay, Ouchterlony, or agglutination assay can be principally used. Among them, EIA is simple and easy to operate with sufficient accuracy and is generally used. By EIA using purified OCIF, the desired antibody can be selected easily and accurately. Thus obtained hybridoma can be cultured by the conventional method of cell culture and frozen for stock if necessary. The antibody can be produced by culturing hybridoma using the ordinary cell culture method or by transplanting hybridoma intraperitoneally to animals. The antibody can be purified by the ordinary purification methods such as salt precipitation, gel filtration, and affinity chromatography. The obtained antibody specifically reacts with OCIF and can be used for determination of OCIF concentration and for purification of OCIF. The antibodies of the present invention recognize epitopes of OCIF and have high affinity to OCIF. Therefore, they can be used for the construction of EIA. By (using) this assay system, the concentration of OCIF in biological materials such as blood and ascites can be easily determined.

The agents used for treating bone diseases that contain OCIF as an effective ingredient are provided by the present invention. Rats were subjected to denervation of left forelimb. Test compounds were administered daily after surgery for 14 days. After 2 weeks treatment, the animals were sacrificed and their forelimbs were dissected. Thereafter bones were tested for mechanical strength by three point bending method. OCIF improved mechanical strength of bone in a dose dependent manner.

The OCIF protein of the invention is useful as a pharmaceutical ingredients for treating or improving decreased bone mass in such as osteoporosis, bone diseases such as rheumatism, osteoarthritis, and abnormal bone metabolism in multiple myeloma. The OCIF protein is also useful as an antigen to establish immunological diagnosis of the diseases. Pharmaceutical preparations containing the OCIF protein as an active ingredients are formulated and can be orally or parenterally administered. The preparation contains the OCIF protein of the present invention as an efficacious ingredient and is safely administered to human and animals. Examples of the pharmaceutical preparations include compositions for injection or intravenous drip, suppositories, nasal preparations, sublingual preparations, and tapes for percutaneous absorption. The pharmaceutical preparation for injection can be prepared by mixing the pharmacologically efficacious amount of OCIF protein and pharmaceutically acceptable carriers. The carriers are vehicles and/or activators, e.g. amino acids, saccharides, cellulose derivatives, and other organic and inorganic compounds which are generally added to active ingredients. When the OCIF protein is mixed with the vehicles and/or activators to prepare injections, pH adjuster, buffer, stabilizer, solubilizing agent, etc. can be added, if necessary.

Brief description of the figures

- 15 Figure 1 shows the elution pattern of crude OCIF protein (HiLoad-Q/FF pass-through fraction ; sample 3) from a HiLoad-S/HP column.
 Figure 2 shows the elution pattern of crude OCIF protein (heparin-5PW fraction ; sample 5) from a blue-5PW column.
 20 Figure 3 shows the elution pattern of OCIF protein (blue-5PW fraction 49 to 50) from a reverse-phase column.
 Figure 4 shows the SDS-PAGE of isolated OCIF proteins under reducing conditions or non-reducing conditions.

Description of the lanes,

- 25 lane 1,4 ; molecular weight marker proteins
 lane 2,5 ; OCIF protein of peak 6 in figure 3
 lane 3,6 ; OCIF protein of peak 7 in figure 3

- Figure 5 shows the elution pattern of peptides obtained by the digestion of pyridyl ethylated OCIF protein digested with lysylendopeptidase, on a reverse-phase column.
 30 Figure 6 shows the SDS-PAGE of isolated natural(n) OCIF protein and recombinant(r) OCIF proteins under non-reducing conditions. rOCIF(E) and rOCIF(C) were produced in 293/EBNA cells and in CHO cells, respectively.

Description of the lanes,

- 35 lane 1 ; molecular weight marker proteins
 lane 2 ; a monomer type nOCIF protein
 lane 3 ; a dimer type nOCIF protein
 lane 4 ; a monomer type rOCIF(E) protein
 lane 5 ; a dimer type rOCIF(E) protein
 lane 6 ; a monomer type rOCIF(C) protein
 40 lane 7 ; a dimer type rOCIF(C) protein

- Figure 7 shows the SDS-PAGE of isolated natural(n) OCIF proteins and recombinant (r) OCIF proteins under reducing conditions. rOCIF(E) and rOCIF(C) were produced in 293/EBNA cells and in CHO cells, respectively.

Description of the lanes,

- 45 lane 8 ; molecular weight marker proteins
 lane 9 ; a monomer type nOCIF protein
 lane 10 ; a dimer type nOCIF protein
 lane 11 ; a monomer type rOCIF(E) protein
 50 lane 12 ; a dimer type rOCIF(E) protein
 lane 13 ; a monomer type rOCIF(C) protein
 lane 14 ; a dimer type rOCIF(C) protein

- 55 Figure 8 shows the SDS-PAGE of isolated natural(n) OCIF proteins and recombinant(r) OCIF proteins from which N-linked sugar chains were removed under reducing conditions. rOCIF(E) and rOCIF(C) are rOCIF protein produced in 293/EBNA cells and in CHO cells, respectively.

Description of the lanes,

- lane 15 ; molecular weight marker proteins
 lane 16 ; a monomer type nOCIF protein
 lane 17 ; a dimer type nOCIF protein
 lane 18 ; a monomer type rOCIF(E) protein
 lane 19 ; a dimer type rOCIF(E) protein
 lane 20 ; a monomer type rOCIF(C) protein
 lane 21 ; a dimer type rOCIF(C) protein

Figure 9 shows comparison of amino acid sequences between OCIF and OCIF2.
 Figure 10 shows comparison of amino acid sequences between OCIF and OCIF3.
 Figure 11 shows comparison of amino acid sequences between OCIF and OCIF4.
 Figure 12 shows comparison of amino acid sequences between OCIF and OCIF5.
 Figure 13 shows standard curve for determination of OCIF protein concentration by an EIA employing anti-OCIF polyclonal antibodies.
 Figure 14 shows standard curve for determination of OCIF protein concentration by an EIA employing anti-OCIF monoclonal antibodies.
 Figure 15 shows the effect of rOCIF protein on osteoporosis.

Best Mode for Carrying Out the Invention

The present invention will be further explained by the following examples, however, the scope of the invention is not restricted to the examples.

EXAMPLE 1

Preparation of a conditioned medium of human fibroblast IMR-90

Human fetal lung fibroblast IMR-90 (ATCC-CCL186) cells were cultured on alumina ceramic pieces (80 g) (alumina: 99.5%, manufactured by Toshiba Ceramic K.K.) in DMEM medium (manufactured by Gibco BRL Co.) supplemented with 5% CS and 10mM HEPES buffer (500 ml/roller bottle) at 37°C under the presence of 5% CO₂ for 7 to 10 days using 60 roller bottles (490 cm², 110 x 171mm, manufactured by Coning Co.) in static culture. The conditioned medium was harvested, and a fresh medium was added to the roller bottles. About 30L of IMR-90 conditioned medium per batch culture was obtained. The conditioned medium was designated as sample 1.

EXAMPLE 2

Assay method for osteoclast development inhibitory activity

Osteoclast development inhibitory activity was assayed by measuring tartrate-resistant acid phosphatase(TRAP) activity according to the methods of M. Kumegawa et.al (Protein • Nucleic Acid • Enzyme, vol.34 p999, 1989) and N. Takahashi et.al (Endocrinology, vol.122, p1373, 1988) with modifications. Briefly, bone marrow cells obtained from 17 day-old mouse were suspended in α-MEM (manufactured by GIBCO BRL Co.) containing 10% FBS, 2x10⁻⁸M of activated vitamin D₃, and each test sample, and were inoculated to each well of 96-well plate at a cell density of 3x10⁵ cells/0.2 ml/well. The plates were incubated for 7 days at 37°C in humidified 5%CO₂. Cultures were further continued by replacing 0.16 ml of old medium with the same volume of fresh medium on day 3 and day 5 after starting cultivation. On day 7, after washing the plates with phosphate buffered saline, cells were fixed with ethanol/acetone (1:1) for 1 min. at room temperature, and then osteoclast development was tested by determining for phosphatase activity using a kit (Acid Phosphatase, Leucocyte, Catalog No. 387-A, manufactured by Sigma Co.). The decrease of TRAP positive cells was taken as an indication of OCIF activity.

EXAMPLE 3

Purification of OCIF

i) Heparin Sepharose CL-6B column chromatography

The 90L of IMR-90 conditioned medium (sample 1) was filtrated with 0.22 μ membrane filter (hydrophilic Millidisk, 2000 cm², Milipore Co.), and was divided into three portions. Each portion (30 l) was applied to a heparin Sepharose

CL-6B column (5 x 4.1 cm, Pharmacia Co.) equilibrated with 10mM Tris-HCl containing 0.3M NaCl, pH 7.5. After washing the column with 10mM Tris-HCl, pH 7.5 at a flow rate of 500 ml/hr., heparin Sepharose CL-6B adsorbent protein fraction was eluted with 10mM Tris-HCl, pH 7.5, containing 2M NaCl. The fraction was designated as sample 2.

5 ii) HiLoad-Q/FF column chromatography

The heparin Sepharose-adsorbent fraction (sample 2) was dialyzed against 10mM Tris-HCl, pH 7.5, supplemented with CHAPS to a final concentration of 0.1%, incubated at 4 °C overnight, and divided into two portions. Each portion was then applied to an anion-exchange column (HiLoad-Q/FF, 2.6 x 10 cm, Pharmacia Co.) which was equilibrated with 10mM Tris-HCl, 0.1% CHAPS, pH 7.5 to obtain a non-adsorbent fraction (1000 ml). The fraction was designated as sample 3.

10 iii) HiLoad-S/HP column chromatography

15 The HiLoad-Q non-adsorbent fraction (sample 3) was applied to a cation-exchange column (HiLoad-S/HP, 2.6 x 10 cm, Pharmacia Co.) which was equilibrated with 50 mM Tris-HCl, 0.1% CHAPS, pH 7.5. After washing the column with 50 mM Tris-HCl, 0.1% CHAPS, pH 7.5, the adsorbed protein was eluted with linear gradient from 0 to 1 M NaCl at a flow rate of 8 ml/min for 100 min. and fractions (12 ml) were collected. Each ten fractions from number 1 to 40 was pooled to form one portion. Each 100 µl of the four portions was tested for OCIF activity. OCIF activity was observed in 20 fractions from 11 to 30 (as shown in Figure 1). The fractions from 21 to 30 which had higher specific activity were collected and was designated as sample 4.

iv) Heparin-5PW affinity column chromatography

25 One hundred and twenty ml of HiLoad-S fraction from 21 to 30 (sample 4) was diluted with 240 ml of 50 mM Tris-HCl, 0.1% CHAPS, pH 7.5, and applied to heparin-5PW affinity column (0.8 x 7.5 cm, Tosoh Co.) which was equilibrated with 50mM Tris-HCl, 0.1% CHAPS, pH 7.5. After washing the column with 50mM Tris-HCl, 0.1% CHAPS, pH 7.5, the adsorbed protein was eluted with linear gradient from 0 to 2M NaCl at a flow rate of 0.5ml/min for 60 min. and fractions (0.5 ml) were collected. Fifty µl was removed from each fraction to test for OCIF activity. The active fractions, 30 eluted with 0.7 to 1.3M NaCl was pooled and was designated as sample 5.

v) Blue 5PW affinity column chromatography

35 Ten ml of sample 5 was diluted with 190 ml of 50mM Tris-HCl, 0.1% CHAPS, pH 7.5 and applied to a blue-5PW affinity column, (0.5x5 cm, Tosoh Co.) which was equilibrated with 50mM Tris-HCl, 0.1% CHAPS, pH 7.5. After washing the column with 50mM Tris-HCl, 0.1% CHAPS, pH7.5, the adsorbed protein was eluted with a 30 ml linear gradient from 0 to 2M NaCl at a flow rate of 0.5 ml/min., and fractions (0.5 ml) were collected. Using 25 µl of each fraction, OCIF activity was evaluated. The fractions number 49 to 70, eluted with 1.0-1.6M NaCl had OCIF activity.

40 vi) Reverse phase column chromatography

The blue 5PW fraction obtained by collecting fractions from 49 to 50 was acidified with 10µl of 25% TFA and applied to a reverse phase C4 column (BU-300, 2.1x220mm, manufactured by Perkin-Elmer) which was equilibrated with 0.1% of TFA and 25% of acetonitrile. The adsorbed protein was eluted with linear gradient from 25 to 55% acetonitrile at a 45 flow rate of 0.2 ml/min. for 60 min., and each protein peak was collected (Fig.3). One hundred µl of each peak fraction was tested for OCIF activity, and peak 6 and the peak 7 had OCIF activity. The result was shown in Table 1.

50

55

Table 1

Sample	Dilution			
	1/40	1/120	1/360	1/1080
Peak 6	++	++	+	-
Peak 7	++	+	-	-
[++ means OCIF activity inhibiting osteoclast development more than 80%, + means OCIF activity inhibiting osteoclast development between 30% and 80%, and - means no OCIF activity.]				

EXAMPLE 4

Molecular weight of OCIF protein

The two protein peaks (6 and 7) with OCIF activity were subjected to SDS-polyacrylamide gel electrophoresis under reducing and non-reducing conditions. Briefly, 20 μ l of each peak fraction was concentrated under vacuum and dissolved in 1.5 μ l of 10mM Tris-HCl, pH 8, 1mM EDTA, 2.5% SDS, 0.01% bromophenol blue, and incubated at 37°C overnight under non-reducing conditions or under reducing conditions (with 5% of 2-mercaptoethanol). Each 1.0 μ l of sample was then analyzed by SDS-polyacrylamide gel electrophoresis with a gradient gel of 10-15% acrylamide (Pharmacia Co.) and an electrophoresis-device (Fast System, Pharmacia Co.). The following molecular weight marker proteins were used to calculate molecular weight : phosphorylase b (94 kD), bovine serum albumin (67 kD), ovalbumin (43 kD), carbonic anhydrase (30 kD), trypsin inhibitor (20.0 kD), and lactalbumin (14.4 kD). After electrophoresis, protein bands were visualized by silver stain using Phast Silver Stain Kit. The results were shown in Fig. 4.

A protein band with an apparent 60 KD was detected in the peak 6 protein under both reducing and non-reducing conditions. A protein band with an apparent 60 KD was detected under reducing conditions and a protein band with an apparent 120 KD was detected under non-reducing conditions in the peak 7 protein. Therefore, the protein of peak 7 was considered to be a homodimer of the protein of peak 6.

EXAMPLE 5

Thermostability of OCIF

Twenty μ l of sample from the blue-5PW fractions 51 and 52 was diluted to 30 μ l with 10 mM phosphate buffered saline, pH 7.2, and incubated for 10 min. at 70°C or 90 °C, or for 30 min. at 56°C. The heat-treated samples were tested for OCIF activity. The results were shown in Table 2.

Table 2

Sample	Dilution		
	1/300	1/900	1/2700
untreated	++	+	-
70°C, 10 min	+	-	-
56°C, 30 min	+	-	-
90°C, 10 min	-	-	-
[++ means OCIF activity inhibiting osteoclast development more than 80%, + means OCIF activity inhibiting osteoclast development between 30% and 80%, and - means no OCIF activity.]			

EXAMPLE 6

Internal amino acid sequence of OCIF protein

5 Each 2 fractions (1 ml) from No. 51-70 of blue-5PW fraction was acidified with 10 µl of 25% TFA, and was applied to a reverse phase C4 column (BU-300, 2.1x220mm, manufactured by Perkin-Elmer Co.) equilibrated with 25% of acetonitrile containing 0.1 % TFA. The adsorbed protein was eluted with a 12 ml linear gradient of 25 to 55% acetonitrile at a flow rate of 0.2 ml/min, and the protein fractions corresponding to peak 6 and peak 7 were collected, respectively. The protein of each peak was applied to a protein sequencer (PROCISE 494, Perkin-Elmer Co.). However, the N-terminal sequence of the protein of each peak could not be analyzed. Therefore, N-terminal of the protein of each peak was considered to be blocked. So, internal amino acid sequences of these proteins were analyzed.

10 The protein of peak 6 or peak 7 purified by C4-HPLC was concentrated by centrifugation and pyridylethylated under reducing conditions. Briefly, 50 µl of 0.5 M Tris-HCl, pH 8.5, containing 100µg of dithiothreitol, 10mM EDTA, 7 M guanidine-HCl, and 1% CHAPS was added to each samples, and the mixture was incubated overnight in the dark at a room temperature. Each the mixture was acidified with 25% TFA (a final concentration 0.1%) and was applied to a reversed phase C4 column (BU-300, 2.1x30mm, Perkin-Elmer Co.) equilibrated with 20 % acetonitrile containing 0.1 % TFA. The pyridil-ethylated OCIF protein was eluted with a 9 ml linear gradient from 20 to 50% acetonitrile at a flow rate of 0.3 ml/min, and each protein peak was collected. The pyridil-ethylated OCIF protein was concentrated under vacuum , and dissolved in 25µl of 0.1 M Tris-HCl, pH 9, containing 8 M Urea, and 0.1 % Tween 80. Seventy three µl of 0.1 M Tris-HCl, pH 9, and 0.02 µg of lysyl endopeptidase (Wako Pure Chemical, Japan) were added to the tube, and incubated at 37 °C for 15 hours. Each digest was acidified with 1 µl of 25% TFA and was applied to a reverse phase C8 column (RP-300, 2.1x220mm, Perkin-Elmer Co.) equilibrated with 0.1% TFA.

15 The peptide fragments were eluted from the column with linear gradient from 0 to 50 % acetonitrile at a flow rate of 0.2 ml/min for 70 min., and each peptide peak was collected. Each peptide fragment (P1 - P3) was applied to the protein sequencer. The sequences of the peptides were shown in Sequence Numbers 1 - 3, respectively.

EXAMPLE 7

Determination of nucleotide sequence of the OCIF cDNA

20 i) Isolation of poly(A) + RNA from IMR-90 cells

25 About 10 ug of poly(A) + RNA was isolated from 1×10^8 cells of IMR-90 by using Fast Track mRNA isolation kit (Invitrogen) according to the manufacturer's instructions.

30 ii) Preparation of mixed primers

35 The following two mixed primers were synthesized based on the amino acid sequences of two peptides (peptide P2 and peptide P3, sequence numbers 2 and 3, respectively). All the oligonucleotides in the mixed primers No. 2F can code for the amino acid sequence from the sixth residue, glutamine (Gln) to the twelfth residue, leucine (Leu), in peptide P2. All the oligonucleotides in the mixed primers No. 3R can code for the amino acid sequence from the sixth residue, histidine (His), to the twelfth residue, lysine (Lys), in peptide P3. The sequences of the mixed primers No. 2F and No. 3R were shown in Table 3.

45

50

55

Table 3

5

No. 2F

10 5' -CAAGAACAAA CTTTCAATT-3'
 G G G C C GC
 A
15 G

20 No. 3R

25 5' -TTTATACATT GTAAAAGAAT G-3'
 C G C G GCTG
 A C
 G T
30

35 iii) Amplification of OCIF cDNA fragment by PCR (Polymerase chain reaction)

First strand cDNA was generated using Superscript II cDNA synthesis kit (Gibco BRL) and 1 ug of poly (A) + RNA obtained in the example 7-i) according to the manufacturer's instructions. The DNA fragment encoding OCIF was obtained by PCR using the cDNA template and the primers shown in EXAMPLE 7-ii).

40 PCR was performed with the conditions as follows;

	10X Ex Taq Buffer (Takara Shuzo)	5 ul
45	2.5 mM solution of dNTPs	4 ul
	cDNA solution	1 ul
	Ex Taq (Takara Shuzo)	0.25 ul
	sterile distilled water	29.75 ul
50	40 uM solution of primers No. 2F	5 ul
	40 uM solution of primers No. 3R	5 ul

55 The components of the reaction were mixed in a microcentrifuge tube. An initial denaturation step at 95 °C for 3 min was followed by 30 cycles of denaturation at 95°C for 30 sec annealing at 50 °C for 30 sec and extention at 70 °C for 2min. After the amplification, final extention step was performed at 70 °C for 5min. The size of PCR products were determined on a 1.5 % agarose gel electrophoresis. About 400 bp OCIF DNA fragment was obtained.

EXAMPLE 8

Cloning of the OCIF cDNA fragment amplified by PCR and determination of its DNA sequence

- 5 The OCIF cDNA fragment amplified by PCR in EXAMPLE 7-iii) was inserted in the plasmid, pBluescript II SK⁻ using
DNA ligation kit ver. 2 (Takara Shuzo) according to the method by Marchuk, D. et al. (Nucleic Acids Res., vol 19, p1154,
1991). E.coli. DH5 α (Gibco BRL) was transformed with ligation mixture. The transformants were grown and a plasmid
containing the OCIF cDNA (about 400 bp) was purified using the commonly used method. This plasmid was called
pBSOCIF. The sequence of OCIF cDNA in pBSOCIF was determined using Taq Dye Deoxy Terminator Cycle Sequenc-
ing kit (Perkin Elmer). The size of the OCIF cDNA is 397 bp. The OCIF cDNA encodes an amino acid sequence con-
taining 132 residues. The amino acid sequences of the internal peptides (peptide P2 and peptide P3, sequence number
2 and 3, respectively) that were used to design the primers were found at N- or C- terminal side in the amino acid
sequence of the 132 amino acid polypeptide predicted by the 397 bp OCIF cDNA. In addition, the amino acid sequence
of the internal peptide P1 (sequence number 1) was also found in the predicted amino acid sequence of the polypep-
tide. These data show that the 397 bp OCIF cDNA is a portion of the full length OCIF cDNA.

EXAMPLE 9

Preparation of the DNA probe

- 20 The 397 bp OCIF cDNA was prepared according to the conditions described in EXAMPLE 7-iii). The OCIF cDNA
was subjected to a preparative agarose gel electrophoresis. The OCIF cDNA was purified from the gel using QIAEX gel
extraction kit (QIAGEN), labeled with [α ³²P]dCTP using Megaprime DNA labeling system (Amersham) and used to
select a phage containing the full length OCIF cDNA.

EXAMPLE 10

Preparation of the cDNA library

- 30 cDNA was generated using Great Lengths cDNA synthesis kit (Clontech), oligo (dT) primer, [α ³²P]dCTP and 2.5
ug of poly(A) + RNA obtained in the example 7-i) according to the manufacturer's instructions. EcoRI-Sall-NotI adaptor
was ligated to the cDNA. The cDNA was separated from the free adaptor and unincorporated free [α ³²P]dCTP. The
purified cDNA was precipitated with ethanol and dissolved in 10 ul of TE buffer (10 mMTris-HCl (pH8.0), 1 mM EDTA).
The cDNA with the adaptor was inserted in λ ZAP EXPRESS vector (Stratagene) at EcoRI site. The recombinant λ ZAP
35 EXPRESS phage DNA containing the cDNA was in vitro packaged using Gigapack gold II packaging extract (Strata-
gene) and recombinant λ ZAP EXPRESS phage library was prepared.

EXAMPLE 11

40 Screening of recombinant phage

- Recombinant phages obtained in EXAMPLE 10 were infected to E. Coli, XL1-Blue MRF' (Stratagene) at 37 °C for
15 min.. The infected E.coli cells were added to NZY medium containing 0.7 % agar at 50°C and plated on the NZY
45 agar plates. After the plates were incubated at 37 °C overnight, Hybond N (Amersham) were placed on the surface of
plates containing plaques. The membranes were denatured in the alkali solution, neutralized, and washed in 2xSSC
according to the standard protocol. The phage DNA was immobilized on the membranes using UV Crosslink (Strata-
gene). The membranes were incubated in the hybridization buffer (Amersham) containing 100 μ g/ml salmon sperm
DNA at 65°C for 4 hours and then incubated at 65 °C overnight in the same buffer containing 2×10^5 cpm/ml denatured
50 OCIF DNA probe. The membranes were washed twice with 2xSSC and twice with a solution containing 0.1xSSC and
0.1 % SDS at 65 °C for 10 min each time. The positive clones were purified by repeating the screening twice. The puri-
fied λ ZAP EXPRESS phage clone containing about 1.6 kb DNA insert was used in the experiments described below.
This phage was called λ OCIF. The purified λ OCIF and the infected into E. Coli XL1-Blue MRF' (Stratagene) according
to a protocol of λ ZAP EXPRESS cloning kit (Stratagene). The culture broth of infected XL1-Blue MRF' was prepared.
Purified 1OCIF and ExAssist helper phage (Stratagene) were co-infected into E. coli strain XL-1 blue MRF' according
55 to the protocol supplied with the kit. The culture broth of the co-infected XL-1 blue MRF' was added to a culture of E.
coli strain XLOR (Stratagene) to transform them. Thus we obtained a Kanamycin-resistant transformant harboring a
plasmid designated pBKOCIF which is a pBKCMV (Stratagene) vector containing the 1.6 kb insert fragment.
The transformant including the plasmid containing about 1.6 kb OCIF cDNA was obtained by picking up the kanamycin-

resistant colonies. The plasmid was called pBKOCIF. The transformant has been deposited to National Institute of Bio-science and Human-Technology (NIBH), Agency of Industrial Science and Technology as "FERM BP-5267" as pBK/O1F10. A national deposit (Accession number, FERM P-14998) was transferred to the international deposit, on October 25, 1995 according to the Budapest treaty. The transformant pBK/O1F10 was grown and the plasmid pBKOCIF was purified according to the standard protocol.

5
EXAMPLE 1210
Determination of the nucleotide sequence of OCIF cDNA containing the full coding region.15
The nucleotide sequence of OCIF cDNA obtained in EXAMPLE 11 was determined using Taq Dye Deoxy Terminator Cycle Sequencing kit (Perkin Elmer). The primers used were T3, T7 primers (Stratagene) and synthetic primers designed according to the OCIF cDNA sequence. The sequences of these primers are shown in sequence numbers 16 to 29. The nucleotide sequence of the OCIF cDNA is shown in sequence number 6 and the amino acid sequence predicted by the cDNA sequence is shown in sequence number 5.

EXAMPLE 13

20
Production of recombinant OCIF by 293/EBNA cells25
i) Construction of the plasmid for expressing OCIF cDNA30
pBKOCIF containing about 1.6 kb OCIF cDNA was prepared as described in EXAMPLE 11, and digested with restriction enzymes, BamHI and Xhol. The OCIF cDNA insert was cut out, separated by an agarose gel electrophoresis, and purified using QIAEX gel extraction kit (QIAGEN). The purified OCIF cDNA insert was ligated using DNA ligation kit ver. 2 (Takara Shuzo) to the expression vector pCEP4 (Invitrogen) digested with restriction enzymes, BamHI and Xhol. E.coli. DH5 α (Gibco BRL) was transformed with the ligation mixture. The transformants were grown and the plasmid containing the OCIF cDNA (about 1.6 kb) was purified using QIAGEN column (QIAGEN). The expression plasmid pCEPOCIF was precipitated with ethanol, and dissolved in sterile distilled water was used in the experiments described below.35
ii) Transient expression of OCIF cDNA and analysis of the biological activity40
Recombinant OCIF was produced using the expression plasmid, pCEPOCIF prepared in EXAMPLE 13-i) according to the method described below. 8×10^5 cells of 293/EBNA (Invitrogen) were inoculated in each well of the 6-well plate using IMDM containing 10 % fetal calf serum (Gibco BRL). After the cells were incubated for 24 hours, the culture medium was removed and the cells were washed with serum free IMDM. The expression plasmid, pCEPOCIF and lipofectamine (Gibco BRL) were diluted with OPTI-MEM (Gibco BRL) and were mixed, and added to the cells in each well according to the manufacturer's instructions. Three μ g of pCEPOCIF and 12 μ l of lipofectamine were used for each transfection. After the cells were incubated with pCEPOCIF and lipofectamine for 38 hours, the medium was replaced with 1 ml of OPTI-MEM. After the transfected cells were incubated for 30 hours, the conditioned medium was harvested and used for the biological assay. The biological activity of OCIF was analysed according to the method described below. Bone marrow cells obtained from mice, 17 days-old, were suspended in α -MEM (manufactured by GIBCO BRL Co.) containing 10% FBS, 2×10^{-8} M activated vitamin D₃, and each test sample, and were inoculated and cultured for 7 days at 37°C in humidified 5%CO₂ as described in EXAMPLE 2. During incubation, 160 μ l of old medium in each well was replaced with the same volume of the fresh medium containing test sample diluted with 1×10^{-8} M of activated vitamin D₃ and α -MEM containing FBS on day 3 and day 5. On day 7, after washing the wells with phosphate buffered saline, cells were fixed with ethanol/acetone (1:1) for 1 min. and then osteoclast development was tested using acid phosphatase activity measuring kit (Acid Phosphatase, Leucocyte, Catalog No. 387-A, Sigma Co.). The decrease of the 45
50
55
number of TRAP positive cells was taken as an OCIF activity. As result, the conditioned medium showed the same OCIF activity as natural OCIF protein from IMR-90 conditioned medium (Table 4).

Table 4

OCIF activity of 293/EBNA conditioned medium.							
	Cultured Cell	Dilution					
		1/20	1/40	1/80	1/160	1/320	1/640
5	OCIF expression vector transfected	++	++	++	++	++	+
10	vector transfected	-	-	-	-	-	-
15	untreated	-	-	-	-	-	-
[++ ; OCIF activity inhibiting osteoclast development more than 80%, + ; OCIF activity inhibiting osteoclast development between 30% and 80%, and - ; no OCIF activity.]							

iii) Isolation of recombinant OCIF protein from 293/EBNA-conditioned medium

293/EBNA-conditioned medium (1.8 l) obtained by cultivating the cells described in example 13-ii) was supplemented with 0.1 % of CHAPS and filtrated with 0.22 µm membrane filter (Stereobecs GS, Milipore Co.). The conditioned medium was applied to 50 ml of a heparin Sepharose CL-6B column (2.6 x 10 cm, Pharmacia Co.) equilibrated with 10mM Tris-HCl, pH 7.5. After washing the column with 10mM Tris-HCl, pH 7.5, the adsorbed protein was eluted from the column with linear gradient from 0 to 2 M NaCl at a flow rate of 4 ml/min for 100 min. and fractions (8 ml) were collected. Using 150 µl of each fraction, OCIF activity was assayed according to the method described in EXAMPLE 2.

25 OCIF active fraction (112 ml) eluted with approximately 0.6 to 1.2 M NaCl was obtained.

One hundred twelve ml of the active fraction was diluted to 1000 ml with 10 mM Tris-HCl, 0.1% CHAPS, pH 7.5, and applied to a heparin affinity column (heparin-5PW, 0.8 x 7.5 cm, Tosoh Co.) equilibrated with 10mM Tris-HCl, 0.1% CHAPS, pH 7.5. After washing the column with 10mM Tris-HCl, 0.1% CHAPS, pH 7.5, the adsorbed protein was eluted from the column with linear gradient from 0 to 2 M NaCl at a flow rate of 0.5ml/min for 60 min., and fractions (0.5 ml) were collected. Four µl of each fraction was analyzed by SDS-polyacrylamide gel electrophoresis under reducing and non-reducing conditions as described in EXAMPLE 4. On SDS-PAGE under reducing conditions, a single band of rOCIF protein with an apparent 60 KD was detected in fractions from 30 to 32, under non-reducing conditions, bands of rOCIF protein with an apparent 60 KD and 120 KD were also detected in fractions from 30 to 32. The isolated rOCIF fraction from 30 to 32 was designated as recombinant OCIF derived from 293/EBNA (rOCIF(E)). 1.5 ml of the rOCIF(E)

35 (535 µg/ml) was obtained when determined by the method of Lowry using bovine serum albumin as a standard protein.

EXAMPLE 14

Production of recombinant OCIF using CHO cells

i) Construction of the plasmid for expressing OCIF

pBKOCIF containing about 1.6 kb OCIF cDNA was prepared as described in EXAMPLE 11, and digested with restriction enzymes, Sall and EcoRV. About 1.4 kb OCIF cDNA insert was separated by an agarose gel electrophoresis, 45 and purified from the gel using QIAEX gel extraction kit (QIAGEN). The expression vector, pcDL-SR α296 (Molecular and Cellular Biology, vol 8, p466, 1988) was digested with restriction enzymes, PstI and KpnI. About 3.4 kb of the expression vector fragment was cut out, separated by agarose gel electrophoresis, and purified from the gel using QIAEX gel extraction kit (QIAGEN). The ends of the purified OCIF cDNA insert and the expression vector fragment were blunted using DNA blunting kit (Takara Shuzo). The purified OCIF cDNA insert and the expression vector fragment 50 were ligated using DNA ligation kit ver. 2 (Takara Shuzo). E.coli. DH5a α (Gibco BRL) was transformed with the ligation mixture. The transformant containing the OCIF expression plasmid, pSRαOCIF was obtained.

ii) Preparation of expression plasmid

55 The transformant containing the OCIF expression plasmid, pSR αOCIF prepared in the example 13-i) and the transformant containing the mouse DHFR expression plasmid, pBAdDSV shown in WO92/01053 were grown according to the standard method. Both plasmids were purified by alkali treatment, polyethylene glycol precipitation, and cesium chrolide density gradient ultra centrifugation according to method of Maniatis et al. (Molecular cloning, 2nd edition).

iii) Adaptation of CHOdhFr- cells to the protein free medium

CHOdhFr- cells (ATCC, CRL 9096) were cultured in IMDM containing 10 % fetal calf serum. The cells were adapted to EX-CELL 301 (JRH Bioscience) and then adapted to EX-CELL PF CHO (JRH Bioscience) according to the manufacturer's instructions.

iv) Transfection of the OCIF expression plasmid, and the mouse DHFR expression plasmid, to CHOdhFr- cells.

CHOdhFr- cells prepared in EXAMPLE 14-iii) were transfected by electroporation with pSRαOCIF and pBAdDSV prepared in EXAMPLE 14-ii). 200 µg of pSRαOCIF and 20 µg of pBAdDSV were dissolved under sterile conditions in 0.8 ml of IMDM (Gibco BRL) containing 10 % fetal calf serum CG. 2x10⁷ cells of CHOdhFr- were suspended in 0.8 ml of this medium. The cell suspension was transferred to a cuvette (Bio Rad) and the cells were transfected by electroporation using gene pulser (Bio Rad) under condition of 360 V and 960 µF. The suspension of electroporated cells was transferred to T-flasks (Sumitomo Bakelite) containing 10 ml of EX-CELL PF-CHO, and incubated in the CO₂ incubator for 2 days. Then the transfected cells were inoculated in each well of a 96 well plate (Sumitomo Bakelite) at a density of 5000 cells/well and cultured for about 2 weeks. The transformants expressing DHFR are selected since EX-CELL PF-CHO does not contain nucleotides and the parental cell line CHO dhFr- can not grow in this medium. Most of the transformants expressing DHFR express OCIF since the OCIF expression plasmid was used ten times as much as the mouse DHFR expression plasmid. The transformants whose conditioned medium had high OCIF activity were selected among the transformants expressing DHFR according to the method described in EXAMPLE 2. The transformants that express large amounts of OCIF were cloned by limiting dilution. The clones whose conditioned medium had high OCIF activity were selected as described above and the transformant expressing large amount of OCIF, 5561, was obtained.

v) Production of recombinant OCIF

To produce recombinant OCIF (rOCIF), EX-CELL 301 medium (3 l) in a 3 l-spiner flask was inoculated with the clone (5561) at a cell-density of 1x10⁵ cells/ml. The 5561 cells were cultured in a spinner flask at 37°C for 4 to 5 days. When the concentration of the 5561 cells reached to 1x10⁶ cells/ml, about 2.7 l of the conditioned medium was harvested. Then about 2.7 l of EX-CELL 301 was added to the spinner flask and the 5561 cells were cultured repeatedly. About 20 l of the conditioned medium was harvested using the three spinner flasks.

vi) Isolation of recombinant OCIF protein from CHO cells-conditioned medium

CHOcells-conditioned medium (1.0 l) described in EXAMPLE 14-v) was supplemented with 1.0 g of CHAPS and filtrated with 0.22 µm membrane filter (Stereobicks GS, Milipore Co.). The conditioned medium was applied to a heparin Sepharose-FF column (2.6 x 10 cm, Pharmacia Co.) equilibrated with 10 mM Tris-HCl, pH 7.5. After washing the column with 10 mM Tris-HCl, 0.1 % CHAPS, pH 7.5, the adsorbed protein was eluted from the column with linear gradient from 0 to 2 M NaCl at a flow rate of 4 ml/min for 100 min. and fractions (8 ml) were collected. Using 150 µl of each fraction, OCIF activity was assayed according to the method described in EXAMPLE 2. Active fraction (112 ml) eluted with approximately 0.6 to 1.2 M NaCl was obtained.

The 112 ml of active fraction was diluted to 1200 ml with 10 mM Tris-HCl, 0.1% CHAPS, pH 7.5, and applied to a affinity column (blue-5PW, 0.5 x 5.0 cm, Tosoh Co.) equilibrated with 10 mM Tris-HCl, 0.1% CHAPS, pH 7.5. After washing the column with 10 mM Tris-HCl, 0.1% CHAPS, pH 7.5, the adsorbed protein was eluted from the column with linear gradient from 0 to 3 M NaCl at a flow rate of 0.5ml/min for 60 min., and fractions (0.5 ml) were collected. Four µl of each fraction was subjected to SDS-polyacrylamide gel electrophoresis under reducing and non-reducing conditions as described in EXAMPLE 4. On SDS-PAGE under reducing conditions, a single band of rOCIF protein with apparent 60 KD was detected in fractions 30 to 38, under non-reducing conditions, bands of rOCIF protein with apparent 60 KD and 120 KD were also detected in fractions 30 to 38. The isolated rOCIF fraction, 30 to 38, was designated as purified recombinant OCIF derived from CHO cells (rOCIF(C)). 4.5 ml of the rOCIF(C) (113 µg/ml) was obtained when determined by the method of Lowry using bovine serum albumin as a standard protein.

EXAMPLE 15

Determination of N-terminal amino acid sequence of rOCIFs

Each 3 µg of the isolated rOCIF(E) and rOCIF(C) was adsorbed to polyvinylidene difluoride (PVDF) membranes with Prospin (PERKIN ELMER Co.). The membranes were washed with 20 % ethanol and the N-terminal amino acid sequences of the adsorbed proteins were analyzed by protein sequencer (PROCISE 492, PERKIN ELMER Co.). The

determined N-terminal amino acid sequence is shown in sequence No. 7.

The N-terminal amino acid of rOCIF(E) and rOCIF(C) was the 22th amino acid of glutamine from Met as translation starting point, as shown in sequence number 5. The 21 amino acids from Met to Gln were identified as a signal peptide. The N-terminal amino acid sequence of OCIF isolated from IMR-90 conditioned medium was undetectable. Accordingly, the N-terminal glutamine of OCIF may be blocked by converting from glutamine to pyroglutamine within culturing or purifying.

EXAMPLE 16

10 Biological activity of recombinant(r) OCIF and natural(n) OCIF

i) Inhibition of vitamin D₃ induced osteoclast formation from murine bone marrow cells

Each the rOCIF(E) and nOCIF sample was diluted with α-MEM (GIBCO BRL Co.) containing 10% FBS and 2x10⁻⁸M of activated vitamin D₃ (a final concentration of 250 ng/ml). Each sample was serially diluted with the same medium, and 100 μl of each diluted sample was added to each well in 96-well plates. Bone marrow cells obtained from mice, 17 days-old, were inoculated at a cell density of 3x10⁵ cells/100μl/well to each well in 96-well plates and cultured for 7 days at 37°C in humidified 5%CO₂. On day 7, the cells were fixed and stained with a acid phosphatase measuring kit (Acid Phosphatase, Leucocyte, No387-A, Sigma) according to the method described in EXAMPLE 2. The decrease of acid phosphatase activity (TRAP) was taken as OCIF activity. The decrease of acid phosphatase-positive cells was evaluated by solubilizing the pigment of dye and measuring absorbance. In detail, 100 μl of a mixture of 0.1 N NaOH and dimethylsulfoxide (1:1) was added to each well and the well was vibrated to solubilize the dye. After solubilizing the dye completely, an absorbance of each well was measured at 590 nm subtracting the absorbance at 490 nm using microplate reader (Immunoreader NJ-2000, InterMed). The microplate reader was adjusted to 0 absorbance using a well with monolayered bone marrow cells which was cultured in the medium without activated vitamin D₃. The decrease of TRAP activity was expressed as a percentage of the control absorbance value (=100%) of the solubilized dye from wells with bone marrow cells which were cultured in the absence of OCIF. The results are shown in Table 5.

30 Table 5

Inhibition of vitamin D3-induced osteoclast formation from murine bone marrow cells						
OCIF concentra-tion(ng/ml)	250	125	63	31	16	0
rOCIF(E)	0	0	3	62	80	100
nOCIF	0	0	27	27	75	100 (%)

40 Both nOCIF and rOCIF(E) inhibited osteoclast formation in a dose dependent manner in the concentration of 16 ng/ml or higher

ii) Inhibition of vitamin D3-induced osteoclast formation in co-cultures of stromal cells and mouse spleen cells.

45 Effect of OCIF on osteoclast formation induced by Vitamin D₃ in co-cultures of stromal cells and mouse spleen cells was tested according to the method of N. Udagawa et al. (Endocrinology, vol. 125, p1805-1813, 1989). In detail, each of rOCIF(E), rOCIF(C), and nOCIF sample was serially diluted with α-MEM (GIBCO BRL Co.) containing 10% FBS, 2x10⁻⁸M of activated vitamin D₃, and 2x10⁻⁷M dexamethasone, and 100μl of each the diluted samples was added to each well in 96 well-microwell plates. Murine bone marrow-derived stromal ST2 cells (RIKEN Cell Bank RCB0224) ; 50 5x10³ cells per 100μl of α-MEM containing 10% FBS, and spleen cells from ddY mice, 8 weeks-old, ; 1x10⁵ cells per 100 μl in the same medium, were inoculated to each well in 96-well plates and cultured for 5 days at 37°C in humidified 5%CO₂. On day 5, the cells were fixed and stained with a kit for acid phosphatase (Acid Phosphatase, Leucocyte, No387-A, Sigma). The decrease of acid phosphatase-positive cells was taken as OCIF activity. The decrease of acid phosphatase-positive cells was evaluated according to the method described in EXAMPLE 16-i). The results are shown 55 in Table 6 ; rOCIF(E) and rOCIF(C), and Table 7 ; rOCIF(E) and nOCIF.

Table 6

Inhibition of osteoclast formation in co-cultures of stromal cells and mouse spleen cells.					
OCIF concentration(ng/ml)	50	25	13	6	0
rOCIF(E)	3	22	83	80	100
rOCIF(C)	13	19	70	96	100 (%)

Table 7

Inhibition of osteoclast formation in co-cultures of stromal cells and mouse spleen cells.				
OCIF concentration(ng/ml)	250	63	16	0
rOCIF(E)	7	27	37	100
rOCIF(C)	13	23	40	100 (%)

nOCIF, rOCIF(E) and rOCIF(C) inhibited osteoclast formation in a dose dependent manner in the concentration of 6 - 16 ng/ml or higher

iii) Inhibition of PTH-induced osteoclast formation from murine bone marrow cells.

Effect of OCIF on osteoclast formation induced by PTH was tested according to the method of N. Takahashi et al. (Endocrinology, vol. 122, p1373-1382, 1988). In detail, each the rOCIF(E) and nOCIF sample (125 ng/ml) was serially diluted with α -MEM (manufactured by GIBCO BRL Co.) containing 10% FBS and 2×10^{-8} M PTH, and 100 μ l of each the diluted samples was added to 96 well-plates. Bone marrow cells from ddY mice, 17 days-old, at a cell density of 3×10^5 cells per 100 μ l of α -MEM containing 10% FBS were inoculated to each well in 96-wells plates and cultured for 5 days at 37°C in humidified 5%CO₂. On day 5, the cells were fixed with ethanol/aceton (1:1) for 1 min. at room temperature and stained with a kit for acid phosphatase (Acid Phosphatase, Leucocyte, No387-A, Sigma) according to the method described in EXAMPLE 2. The decrease of acid phosphatase-positive cells was taken as OCIF activity. The decrease of acid phosphatase-positive cells was evaluated according to the method described in EXAMPLE 16-i). The results are shown in Table 8.

Table 8

Inhibition of PTH-induced osteoclast formation from murine bone marrow cells.						
OCIF concentration(ng/ml)	125	63	31	16	8	0
rOCIF(E)	6	58	58	53	88	100
nOCIF	18	47	53	56	91	100

nOCIF and rOCIF(E) inhibited osteoclast formation in a dose dependent manner in the concentration of 16 ng/ml or higher

iv) Inhibition of IL-11-induced osteoclast formation

Effect of OCIF on osteoclast formation induced by IL-11 was tested according to the method of T. Tamura et al. (Proc. Natl. Acad. Sci. USA, vol. 90, p11924-11928, 1993). In detail, each rOCIF(E) and nOCIF sample was serially

diluted with α -MEM (GIBCO BRL Co.) containing 10% FBS and 20 ng/ml IL-11 and 100 μ l of each the diluted sample was added to each well in 96-well plates. Newborn mouse calvaria-derived pre-adipocyte MC3T3-G2/PA6 cells (RIKEN Cell Bank RCB1127) ; 5x10³ cells per 100 μ l of α -MEM containing 10% FBS, and spleen cells from ddy mouse, 8 weeks-old, ; 1x10⁵ cells per 100 μ l in the same medium, were inoculated to each well in 96-well plates and cultured for 5 days at 37 °C in humidified 5%CO₂. On day 5, the cells were fixed and stained with a kit for acid phosphatase (Acid Phosphatase, Leucocyte, No387-A, Sigma). Acid phosphatase positive cells were counted under microscope and a decrease of the cell numbers was taken as OCIF activity. The results are shown in Table 9.

Table 9

OCIF concentration(ng/ml)	500	125	31	7.8	2.0	0.5	0
nOCIF	0	0	1	4	13	49	31
rOCIF(E)	0	0	1	3	10	37	31
Both nOCIF and rOCIF(E) inhibited osteoclast formation in a dose dependent manner in the concentration of 2 ng/ml or higher							

The results shown in Table 4-8 indicated that OCIF inhibits all the vitamin D₃, PTH, and IL-11-induced osteoclast formations at almost the same doses. Accordingly, OCIF would be able to be used for treatment of the different types of bone disorders with decreased bone mass, which are caused by different substances which induce bone resorption.

EXAMPLE 17

Isolation of monomer-type OCIF and dimer-type OCIF

Each rOCIF(E) and rOCIF(C) sample containing 100 μ g of OCIF protein, was supplemented with 1/100 volume of 25 % trifluoro acetic acid and applied to a reverse phase column (PROTEIN-RP, 2.0x250 mm, YMC Co.) equilibrated with 30 % acetonitrile containing 0.1 % trifluoro acetic acid. OCIF protein was eluted from the column with linear gradient from 30 to 55 % acetonitrile at a flow rate of 0.2 ml/min for 50 min. and each OCIF peak was collected. Each the monomer-type OCIF peak fraction and dimer-type OCIF peak fraction was lyophilized, respectively.

EXAMPLE 18

Determination of molecular weight of recombinant OCIFs

Each 1 μ g of the isolated monomer-type and dimer-type nOCIF purified using reverse phase column according to EXAMPLE 3-iv) and each 1 μ g of monomer-type and dimer-type rOCIF described in EXAMPLE 17 was concentrated under vaccum, respectively. Each sample was incubated in the buffer for SDS-PAGE, subjected to SDS-polyacrylamide gel electrophoresis, and protein bands on the gel were stained with silver according to the method described in EXAMPLE 4. Results of electrophoresis under non-reducing conditions and reducing conditions are shown in Figure 6 and Figure 7.

A protein band with an apparent molecular weight of 60 KD was detected in each monomer-type OCIF sample, and a protein band with an apparent molecular weight of 120 KD was detected in each dimer-type OCIF sample in non-reducing conditions. A protein band with an apparent molecular weight of 60 KD was detected in each monomer-type OCIF sample under reducing conditions. Accordingly, molecular weights of monomer-type nOCIF from IMR-90 cells, rOCIF from 293/EBNA cells and rOCIF from CHO cells were almost the same. Molecular weights of dimer-type nOCIF from IMR-90 cells, rOCIF from 293/EBNA cells, and rOCIF from CHO cells were also the same.

EXAMPLE 19

Remove N-linked Oligosaccharide chain and Mesuring molecular weight of natural and recombinant OCIF

Each sample containing 5 μ g of the isolated monomer-type and dimer-type nOCIF purified using reverse phase column according to EXAMPLE 3-iv) and each sample containing 5 μ g of monomer-type and dimer-type rOCIF described in EXAMPLE 17 were concentrated under vaccum. Each sample was dissolved in 9.5 μ l of 50 mM sodium phosphate buffer, pH 8.6, containing 100 mM 2-mercaptoethanol, supplemented with 0. 5 μ l of 250 U/ml N-glycanase (Seikagaku

kogyo Co.) and incubated for one day at 37 °C. Each sample was supplemented with 10 µl of 20 mM Tris-HCl, pH 8.0 containing 2 mM EDTA, 5 % SDS, and 0.02 % bromo-phenol blue and heated for 5 min at 100 °C. Each 1 µl of the samples was subjected to SDS-polyacrylamide gel electrophoresis, and protein bands on the gel were stained with silver as described in EXAMPLE 4. The patterns of electrophoresis are shown in Figure 8.

5 An apparent molecular weight of each the deglycosylated nOCIF from IMR-90 cells, rOCIF from CHO cells, and rOCIF from 293/EBNA cells was 40 KD under reducing conditions. An apparent molecular weight of each untreated nOCIF from IMR-90 cells, rOCIF from 293/EBNA cells, and rOCIF from CHO cells was 60 KD under reducing conditions. Accordingly, the results indicate that the OCIF proteins are glycoproteins with N-linked sugar chains.

10 EXAMPLE 20

Cloning of OCIF variant cDNAs and determination of their DNA sequences

The plasmid pBKOCIF, which is inserted OCIF cDNA to pBKCMV (Stratagene), was obtained from one of some purified positive phage as in example 10 and 11. And more, during the screening of the cDNA library with the 397 bp OCIF cDNA probe, the transformants containing plasmids whose insert sizes were different from that of pBKOCIF were obtained. These transformants containing the plasmids were grown and the plasmids were purified according to the standard method. The sequence of the insert DNA in each plasmid was determined using Taq Dye Deoxy Terminator Cycle Sequencing kit (Perkin Elmer). The used primers were T3, T7 primers (Stratagene) and synthetic primers prepared based on the nucleotide sequence of OCIF cDNA. There are four OCIF variants (OCIF2, 3, 4, and 5) in addition to OCIF. The nucleotide sequence of OCIF2 is shown in the sequence number 8 and the amino acid sequence of OCIF 2 predicted by the nucleotide sequence is shown in the sequence number 9. The nucleotide sequence of OCIF3 is shown in the sequence number 10 and the amino acid sequence of OCIF3 predicted by the nucleotide sequence is shown in the sequence number 11. The nucleotide sequence of OCIF4 is shown in the sequence number 12 and the amino acid sequence of OCIF4 predicted by the nucleotide sequence is shown in the sequence number 13. The nucleotide sequence of OCIF5 is shown in the sequence number 14 and the amino acid sequence of OCIF5 predicted by the nucleotide sequence is shown in the sequence number 15. The structures of OCIF variants are shown in Figures 9 to 12 and are described in brief below. OCIF2

OCIF2 cDNA has a deletion of 21 bp from guanine at nucleotide number 265 to guanine at nucleotide number 285 in OCIF cDNA (sequence number 6). Accordingly OCIF2 has a deletion of 7 amino acids from glutamic acid (Glu) at amino acid number 68 to glutamine (Gln) at amino acid number 74 in OCIF (sequence number 5).

OCIF3

35 OCIF3 cDNA has a point mutation at nucleotide number 9 in OCIF cDNA (sequence number 6) where cytidine is replaced with guanine.

Accordingly OCIF3 has a mutation and asparagine (Asn) at amino acid number -19 in OCIF (sequence number 5) is replaced with lysine (Lys). The mutation seems to be located in the signal sequence and have no essential effect on the secreted OCIF3. OCIF3 cDNA has a deletion of 117 bp from guanine at nucleotide number 872 to cytidine at nucleotide number 988 in OCIF cDNA (sequence number 6).

Accordingly OCIF3 has a deletion of 39 amino acids from threonine (Thr) at amino acid number 270 to leucine (Leu) at amino acid number 308 in OCIF (sequence number 5).

OCIF4

45 OCIF4 cDNA has two point mutations in OCIF cDNA (sequence number 6). Cytidine at nucleotide number 9 is replaced with guanine and guanine at nucleotide number 22 is replaced with thymidine in OCIF cDNA (sequence number 6).

Accordingly OCIF4 has two mutations. Asparagine (Asn) at amino acid number -19 in OCIF (sequence number 5) is replaced with lysine (Lys), and alanine (Ala) at amino acid number -14 is replaced with serine (Ser). These mutations seem to be located in the signal sequence and have no essential effect on the secreted OCIF4.

OCIF4 cDNA has about 4 kb DNA, which is the intron 2 of OCIF gene, inserted between nucleotide number 400 and nucleotide number 401 in OCIF cDNA (sequence number 6). The open reading frame stops in intron 2.

Accordingly OCIF4 has an additional novel amino acid sequence containing 21 amino acids after alanine (Ala) at amino acid number 112 in OCIF (sequence number 5).

OCIF5

OCIF5 cDNA has a point mutation at nucleotide number 9 in OCIF cDNA (sequence number 6) where cytidine is replaced with guanine.

- 5 Accordingly OCIF5 has a mutation and asparagine (Asn) at amino acid number -19 in OCIF (sequence number 5) is replaced with lysine (Lys). The mutation seems to be located in the signal sequence and have no essential effect on the secreted OCIF5.
- OCIF5 cDNA has the latter portion (about 1.8 kb) of intron 2 between nucleotide number 400 and nucleotide number 401 in OCIF cDNA (sequence number 6). The open reading frame stops in the latter portion of intron 2.
- 10 Accordingly OCIF5 has an additional novel amino acid sequence containing 12 amino acids after alanine (Ala) at amino acid number 112 in OCIF (sequence number 5).

EXAMPLE 21

15 Production of OCIF variants

i) Construction of the plasmid for expressing OCIF variants

- The plasmid containing OCIF2 or OCIF3 cDNA was obtained as described in EXAMPLE 20 and called pBKOCIF2 and pBKOCIF3, respectively. pBKOCIF2 and pBKOCIF3 were digested with restriction enzymes, BamHI and Xhol. The OCIF2 and OCIF3 cDNA inserts were separated by agarose gel electrophoresis, and purified from the gel using QIAEX gel extraction kit (QIAGEN). The purified OCIF2 and OCIF3 cDNA inserts were individually ligated using DNA ligation kit ver. 2 (Takara Shuzo) to the expression vector pCEP4 (Invitrogen) that had been digested with restriction enzymes, BamHI and Xhol. E. coli. DH5 α (Gibco BRL) was transformed with the ligation mixture.
- 25 The plasmid containing OCIF4 cDNA was obtained as described in EXAMPLE 20 and called pBKOCIF4. pBKOCIF4 was digested with restriction enzymes, SphI and Xhol (Takara Shuzo). The OCIF4 cDNA insert was separated by an agarose gel electrophoresis, and purified from the gel using QIAEX gel extraction kit (QIAGEN). The purified OCIF4 cDNA insert was ligated using DNA ligation kit ver. 2 (Takara Shuzo) to the expression vector pCEP4 (Invitrogen) that had been digested with restriction enzymes, NheI and Xhol (Takara Shuzo). E.coli. DH5 α (Gibco BRL) was transformed with the ligation mixture.
- 30 The plasmid containing OCIF5 cDNA was obtained as described in EXAMPLE 20 and was called pBKOCIF5. pBKOCIF5 was digested with restriction enzyme, HindIII (Takara Shuzo). The 5' portion of the coding region in the OCIF5 cDNA insert was separated by agarose gel electrophoresis, and purified from the gel using QIAEX gel extraction kit (QIAGEN). The OCIF expression plasmid, pCEPOCIF, obtained in EXAMPLE 13-i) was digested with restriction enzyme, HindIII (Takara Shuzo). The 5' portion of the coding region in the OCIF cDNA was removed. The rest of the plasmid that contains pCEP vector and the 3' portion of the coding region of OCIF cDNA was called pCEPOCIF-3'. pCEPOCIF-3' was separated by an agarose gel electrophoresis, and purified from the gel using QIAEX gel extraction kit (QIAGEN). The OCIF5 cDNA HindIII fragment and pCEPOCIF-3' were ligated using DNA ligation kit ver. 2 (Takara Shuzo). E.coli. DH5 α (Gibco BRL) was transformed with the ligation mixture.
- 40 The obtained transformants were grown at 37 °C overnight and the OCIF variants expression plasmids (pCEPOCIF2, pCEPOCIF3, pCEPOCIF4, and pCEPOCIF5) were purified using QIAGEN column (QIAGEN). These OCIF-variants-expression plasmids were precipitated with ethanol, dissolved in sterile distilled water, and used in the experiments described below.

45 ii) Transient expression of OCIF variant cDNAs and analysis of the biological activity of recombinant OCIF variants.

- Recombinant OCIF variants were produced using the expression plasmid, pCEPOCIF2, pCEPOCIF3, pCEPOCIF4, and pCEPOCIF5 prepared as described in EXAMPLE 21-i) according to the method described in EXAMPLE 13-ii). The biological activities of recombinant OCIF variants were analyzed. The results were that these OCIF variants (OCIF2, OCIF3, OCIF4, and OCIF5) had a weak activity.

EXAMPLE 22

Preparation of OCIF mutants

- 55 i) Construction of a plasmid vector for subcloning cDNAs encoding OCIF mutants

The plasmid vector (5 μ g) described in EXAMPLE 11 was digested with restriction enzymes Bam HI and Xho I (

Takara Shuzo). The digested DNA was subjected to a preparative agarose gel electrophoresis. DNA fragment with an approximate size of 1.6 kilobase pairs (kb) that contained the entire coding sequence for OCIF was purified from the gel using QIAEX gel extraction kit (QIAGEN). The purified DNA was dissolved in 20 µl of sterile distilled water. This solution was designated DNA solution 1. p Bluescript II SK + (3 µg) (Stratagene) was digested with restriction enzymes Bam HI and Xho I (Takara Shuzo). The digested DNA was subjected to preparative agarose gel electrophoresis. DNA fragment with an approximate size of 3.0 kb was purified from the gel using QIAEX DNA extraction kit (QIAGEN). The purified DNA was dissolved in 20 µl of sterile distilled water. The solution was designated DNA solution 2. One microliter of DNA solution 2, 4 µl of DNA solution 1 and 5 µl of ligation buffer I of DNA ligation kit ver. 2 (Takara Shuzo) were mixed and incubated at 16 °C for 30 min. (The ligation mixture was used for the transformation of E. coli in a manner described below). Conditions for transformation of E. coli were as follows. One hundred microliters of competent E. coli DH5 α cells (GIBCO BRL) and 5 µl of the ligation mixture was mixed in a sterile 15-ml tube (IWAKI glass). The tube was kept on ice for 30 min. After incubation for 45 sec at 42°C, to the cells was added 250 µl of L broth (1% Tryptone, 0.5% yeast extract, 1% NaCl). The cell suspension was then incubated for 1 hr. at 37°C with shaking. Fifty microliters of the cell suspension was plated onto an L-agar plate containing 50 µg/ml of ampicillin. The plate was incubated overnight at 37°C.

Six colonies which grew on the plate were individually incubated in 2 ml each of L-broth containing 50 µg/ml of ampicillin overnight at 37°C with shaking. The structure of the plasmids in the colonies was analyzed. A plasmid in which the 1.6-kb DNA fragment containing the entire OCIF cDNA is inserted between the digestion sites of Bam HI and Xho I of pBluescript II SK + was obtained and designated as pSK + -OCIF.

ii) Preparation of mutants in which one of the Cys residues in OCIF is replaced with Ser residue

1) Introduction of mutations into OCIF cDNA

OCIF mutants were prepared in which one of the five Cys residues present in OCIF at positions 174, 181, 256, 298 and 379 (in SEQUENCE NO 4) was replaced with Ser residue and were designated OCIF-C19S (174Cys to Ser), OCIF-C20S (181Cys to Ser), OCIF-C21S (256Cys to Ser), OCIF-C22S (298Cys to Ser) and OCIF-C23S (379Cys to Ser), respectively.

To prepare the mutants, nucleotides encoding the corresponding Cys residues were replaced with those encoding Ser. Mutagenesis was carried out by a two-step polymerase chain reaction (PCR). The first step of the PCRs consisted of two reactions, PCR 1 and PCR 2.

35	PCR 1	10X Ex Taq Buffer (Takara Shuzo)	10 µl
		2.5 mM solution of dNTPs	8 µl
		the plasmid vector described in EXAMPLE 11 (8ng/ml)	2 µl
		sterile distilled water	73.5 µl
		20 µM solution of primer 1	5 µl
	PCR 2	100 µM solution of primer 2 (for mutagenesis)	1 µl
		Ex Taq (Takara Shuzo)	0.5 µl
		10X Ex Taq Buffer (Takara Shuzo)	10 µl
		2.5 mM solution of dNTPs	8 µl
		the plasmid vector described in EXAMPLE 11 (8ng/ml)	2 µl
40	PCR 2	sterile distilled water	73.5 µl
		20 µM solution of primer 3	5 µl
		100 µM solution of primer 4 (for mutagenesis)	1 µl
		Ex Taq (Takara Shuzo)	0.5 µl

Specific sets of primers were used for each mutation and other components were unchanged. Primers used for the reactions are shown in Table 10. The nucleotide sequences of the primers are shown in SEQUENCE NO: 20, 23, 27 and 30-40. The PCRs were performed under the following conditions as follows. An initial denaturation step at 97°C for 3 min was followed by 25 cycles of denaturation at 95°C for 1 min annealing at 55°C for 1 min and extension at 72°C for

3 min. After these amplification cycles, final extension was performed at 70°C for 5 min. The size of the PCR products was confirmed by agarose gel electrophoresis using reaction solution. After the first PCR, excess primers were removed using Amicon microcon (Amicon). The final volume of the solutions that contained the PCR products were made to 50 µl with sterile distilled water. These purified PCR products were used for the second PCR (PCR 3).

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PCR 3	10X Ex Taq Buffer (Takara Shuzo)	10 µl
	2.5 mM solution of dNTPs	8 µl
	solution containing DNA fragment obtained from PCR 1	5 µl
	solution containing DNA fragment obtained from PCR 2	5 µl
	sterile distilled water	61.5 µl
	20 µM solution of primer 1	5 µl
	20 µM solution of primer 3	5 µl
	Ex Taq (Takara Shuzo)	0.5 µl

Table 10

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mutants	primer-1	primer-2	primer-3	primer-4
OCIF-C19S	IF 10	C19SR	IF 3	C19SF
OCIF-C20S	IF 10	C20SR	IF 3	C20SF
OCIF-C21S	IF 10	C21SR	IF 3	C21SF
OCIF-C22S	IF 10	C22SR	IF 14	C22SF
OCIF-C23S	IF 6	C23SR	IF 14	C23SF

The reaction conditions were exactly the same as those for PCR 1 or PCR 2. The size of the PCR products was confirmed by 1.0 % or 1.5 % agarose gel electrophoresis. The DNA fragments were precipitated with ethanol, dried under vacuum and dissolved in 40 µl of sterile distilled water. The solutions containing DNA fragments with mutation C19S, C20S, C21S, C22S and C23S were designated as DNA solution A, DNA solution B, DNA solution C, DNA solution D and DNA solution E, respectively.

The DNA fragment which is contained in solution A (20 µl) was digested with restriction enzymes Nde I and Sph I (Takara Shuzo). A DNA fragment with an approximate size of 400 base pairs (bp) was extracted from a preparative agarose gel and dissolved in 20 µl of sterile distilled water. This DNA solution was designated DNA solution 3. Two micrograms of pSK + -OCIF was digested with restriction enzymes Nde I and Sph I. A DNA fragment with an approximate size of 4.2 kb was purified from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 µl of sterile distilled water. This DNA solution was designated as DNA solution 4. Two microliters of DNA solution 3, 3 µl of DNA solution 4 and 5 µl of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent *E. coli* DH5 α cells were transformed with 5 µl of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-C19S.

The DNA fragment which is contained in solution B (20 µl) was digested with restriction enzymes Nde I and Sph I. A DNA fragment with an approximate size of 400 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 µl of sterile distilled water. This DNA solution was designated DNA solution 5. Two microliters of DNA solution 5, 3 µl of DNA solution 4 and 5 µl of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent *E. coli* DH5 α cells were transformed with 5 µl of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-C20S.

The DNA fragment which is contained in solution C (20 µl) was digested with restriction enzymes Nde I and Sph I. A DNA fragment with an approximate size of 400 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 µl of sterile distilled water. This DNA solution was designated as DNA solution 6. Two micro-

liters of DNA solution 6, 3 µl of DNA solution 4 and 5µl of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent E. coli DH5 α cells were transformed with 5 µl of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-C21S.

5 The DNA fragment which is contained in solution D (20 µl) was digested with restriction enzymes Nde I and Bst PI. A DNA fragment with an approximate size of 600 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 µl of sterile distilled water. This DNA solution was designated as DNA solution 7. Two micrograms of pSK + -OCIF was digested with restriction enzymes Nde I and Bst PI. A DNA fragment with an approximate size of 4.0 kb was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20µl of sterile distilled water. This DNA solution was designated as DNA solution 8. Two microliters of DNA solution 7, 3 µl of DNA solution 8 and 5µl of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent E. coli DH5 α cells were transformed with 5 µl of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA in which the 600-bp Nde I-BstPI fragment with the mutation (the C22S mutation) is substituted for the 600-bp Nde I-Bst PI fragment of pSK+ -OCIF by analyzing the DNA structure. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-C22S.

10 The DNA fragment which is contained in solution E (20 µl) was digested with restriction enzymes Bst PI and Eco RV. A DNA fragment with an approximate size of 120 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20µl of sterile distilled water. This DNA solution was designated as DNA solution 9. Two micrograms of pSK + -OCIF was digested with restriction enzymes Bst EII and Eco RV. A DNA fragment with an approximate size of 4.5 kb was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20µl of sterile distilled water. This DNA solution was designated as DNA solution 10. Two microliters of DNA solution 9, 3 µl of DNA solution 10 and 5 µl of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation was carried out. Competent E. coli DH5 α cells were transformed with 5µl of the ligation mixture. Ampicillin-resistant transformants were screened 15 for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-C23S.

2) Construction of vectors for expressing the OCIF mutants

30 pSK-OCIF-C19S, pSK-OCIF-C20S, pSK-OCIF-C21S, pSK-OCIF-C22S and pSK-OCIF-C23S were digested with restriction enzymes Bam HI and Xho I. The 1.6 kb Bam HI-Xho I DNA fragment encoding each OCIF mutant was isolated and dissolved in 20µl of sterile distilled water. The DNA solutions that contain 1.6 kb cDNA fragments derived from pSK-OCIF-C19S, pSK-OCIF-C20S, pSK-OCIF-C21S, pSK-OCIF-C22S and pSK-OCIF-C23S were designated C19S DNA solution, C20S DNA solution, C21S DNA solution, C22S DNA solution and C23S DNA solution, respectively. Five 35 micrograms of a expression vector pCEP 4 (Invitrogen) was digested with restriction enzymes Bam HI and Xho I. A DNA fragment with an approximate size of 10 kb was purified and dissolved in 40µl of sterile distilled water. This DNA solution was designated as pCEP 4 DNA solution. One microliter of pCEP 4 DNA solution and 6 µl of either C19SDNA solution, C20S DNA solution, C21S DNA solution, C22S DNA solution or C23S DNA solution were independently mixed with 7 µl of ligation buffer I of DNA ligation kit ver. 2 and ligation reactions were carried out. Competent E. coli 40 DH5 α cells (100µl) were transformed with 7 µl of each ligation mixture. Ampicillin-resistant transformants were screened for clones containing plasmid in which a 1.6-kb cDNA fragment is inserted between the recognition sites of Bam HI and Xho I of pCEP 4 by analyzing the DNA structure. The plasmide which were obtained containing the cDNA encoding OCIF-C19S, OCIF-C20S, OCIF-C21S, OCIF-C22S and OCIF-C23S were designated pCEP4-OCIF-C19S, pCEP4-OCIF-C20S, pCEP4-OCIF-C21S, pCEP4-OCIF-C22S and pCEP4-OCIF-C23S, respectively.

45 ii) Preparation of domain-deletion mutants of OCIF

(1) deletion mutagenesis of OCIF cDNA

50 A series of OCIF mutants with deletions of from Thr 2 to Ala 42, from Pro 43 to Cys 84, from Glu 85 to Lys 122, from Arg 123 to Cys 164, from Asp 177 to Gln 251 and from Ile 252 to His 326 were prepared (positions of the amino acid residues are shown in SEQUENCE NO: 4). These mutants were designated as OCIF-DCR1, OCIF-DCR2, OCIF-DCR3, OCIF-DCR4, OCIF-DDD1 and OCIF-DDD2, respectively.

Mutagenesis was performed by two-step PCR as described in EXAMPLE 22-(ii). The primer sets for the reactions are 55 shown in Table 11 and the nucleotide sequences of the primers are shown in SEQUENCE NO: 19, 25, 40-53, and 54.

Table 11

mutants	primer-1	primer-2	primer-3	primer-4
OCIF-DCR1	Xhol F	DCR1R	IF 2	DCR1F
OCIF-DCR2	Xhol F	DCR2R	IF 2	DCR2F
OCIF-DCR3	Xhol F	DCR3R	IF 2	DCR3F
OCIF-DCR4	Xhol F	DCR4R	IF 16	DCR4F
OCIF-DDD1	IF 8	DDD1R	IF 14	DDD1F
OCIF-DDD2	IF 8	DDD2R	IF 14	DDD2F

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The final PCR products were precipitated with ethanol, dried under vacuum and dissolved in 40 μ l of sterile distilled water. Solutions of DNA fragment coding for portions of OCIF-DCR1, OCIF-DCR2, OCIF-DCR3, OCIF-DCR4, OCIF-DDD1 and OCIF-DDD2 were designated as DNA solutions F, G, H, I, J and K, respectively.

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The DNA fragment which is contained in solution F (20 μ) was digested with restriction enzymes Nde I and Xho I. A DNA fragment with an approximate size of 500 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 μ l of sterile distilled water. This DNA solution was designated DNA solution 11. Two micrograms of pSK+ -OCIF was digested with restriction enzymes Nde I and Xho I. A DNA fragment with an approximate size of 4.0 kb was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 μ l of sterile distilled water. This DNA solution was designated DNA solution 12. Two microliters of DNA solution 11, 3 μ l of DNA solution 12 and 5 μ l of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation was carried out. Competent E. coli DH5 α cells were transformed with 5 μ l of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-DCR1.

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The DNA fragment which is contained in solution G (20 μ) was digested with restriction enzymes Nde I and Xho I.

A DNA fragment with an approximate size of 500 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 μ l of sterile distilled water. This DNA solution was designated as DNA solution 13. Two microliters of DNA solution 13, 3 μ l of DNA solution 12 and 5 μ l of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation was carried out. Competent E. coli DH5 α cells were transformed with 5 μ l of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-DCR2.

The DNA fragment which is contained in solution H (20 μ) was digested with restriction enzymes Nde I and Xho I. A DNA fragment with an approximate size of 500 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 μ l of sterile distilled water. This DNA solution was designated as DNA solution 14. Two microliters of DNA solution 14, 3 μ l of DNA solution 12 and 5 μ l of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent E. coli DH5 α cells were transformed with 5 μ l of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-DCR3.

The DNA fragment which is contained in solution I (20 μ) was digested with restriction enzymes Xho I and Sph I. A DNA fragment with an approximate size of 900 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 μ l of sterile distilled water. This DNA solution was designated as DNA solution 15. Two micrograms of pSK+ -OCIF was digested with restriction enzymes Xho I and Sph I. A DNA fragment with an approximate size of 3.6 kb was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 μ l of sterile distilled water. This DNA solution was designated as DNA solution 16. Two microliters of DNA solution 15, 3 μ l of DNA solution 16 and 5 μ l of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent E. coli DH5 α cells were transformed with 5 μ l of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-DCR4.

The DNA fragment which is contained in solution J (20 μ) was digested with restriction enzymes BstP I and Nde I. A DNA fragment with an approximate size of 400 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 μ l of sterile distilled water. This DNA solution was designated as DNA solution 17. Two microliters of DNA solution 17, 3 μ l of DNA solution 8 and 5 μ l of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent E. coli DH5 α cells were transformed with 5 μ l of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by

restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-DDD1. The DNA fragment which is contained in solution K (20 µl) was digested with restriction enzymes Nde I and BstP I. A DNA fragment with an approximate size of 400 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 µl of sterile distilled water. This DNA solution was designated as DNA solution 18. Two microliters of DNA solution 18, 3 µl of DNA solution 8 and 5µl of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent E. coli DH5 α cells were transformed with 5 µl of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-DDD2.

10 2) Construction of vectors for expressing the OCIF mutants

pSK-OCIF-DCR1, pSK-OCIF-DCR2, pSK-OCIF-DCR3, pSK-OCIF-DCR4, pSK-OCIF-DDD1 and pSK-OCIF-DDD2 were digested with restriction enzymes Bam HI and Xho I. The Bam HI-Xho I DNA fragment containing entire coding sequence for each OCIF mutant was isolated and dissolved in 20 µl of sterile distilled water. These DNA solutions that 15 contain the Bam HI-Xho I fragment derived from pSK-OCIF-DCR1, pSK-OCIF-DCR2, pSK-OCIF-DCR3, pSK-OCIF-DCR4, pSK-OCIF-DDD1 and pSK-OCIF-DDD2 were designated DCR1 DNA solution, DCR2 DNA solution, DCR3 DNA solution, DCR4 DNA solution, DDD1 DNA solution and DDD2 DNA solution, respectively. One microliter of pCEP 4 DNA solution and 6µl of either DCR1 DNA solution, DCR2 DNA solution, DCR3 DNA solution, DCR4 DNA solution, DDD1 DNA solution or DDD2 DNA solution were independently mixed with 7µl of ligation buffer I of DNA ligation kit ver. 20 2 and ligation reactions were carried out. Competent E. coli DH5 α cells (100 µl) were transformed with 7 µl of each ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA in which the DNA structure. The plasmids containing the cDNA encoding OCIF-DCR1, OCIF-DCR2, OCIF-DCR3, OCIF-DCR4, OCIF-DDD1 and OCIF-DDD2 were designated as pCEP4-OCIF-DCR1, pCEP4-OCIF-DCR2, pCEP4-OCIF-DCR3, pCEP4-OCIF-DCR4, pCEP4-OCIF-DDD1 and pCEP4-OCIF-DDD2, respectively.

25 iii) Preparation of OCIF with C-terminal domain truncation

(1) mutagenesis of OCIF cDNA

30 A series of OCIF mutants with deletions of from Cys at amino acid residue 379 to Leu 380, from Ser 331 to Leu 380, from Asp 252 to Leu 380, from Asp 177 to Leu 380, from Arg 123 to Leu 380 and from Cys 86 to Leu 380 was prepared. Positions of the amino acid residues are shown in SEQUENCE NO: 4. These mutants were designated as OCIF-CL, OCIF-CC, OCIF-CDD2, OCIF-CDD1, OCIF-CCR4 and OCIF-CCR3, respectively.

35 Mutagenesis for OCIF-CL was performed by the two-step PCR as described in EXAMPLE 22-(ii). The primer set for the reaction is shown in Table 12. The nucleotide sequences of the primers are shown in SEQUENCE NO:23, 40, 55, and 56. The final PCR products were precipitated with ethanol, dried under vacuum and dissolved in 40µl of sterile distilled water. This DNA solution was designated as solution L.

The DNA fragment which is contained in solution L (20 µl) was digested with restriction enzymes BstP I and EcoR 40 V. A DNA fragment with an approximate size of 100 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20µl of sterile distilled water. This DNA solution was designated as DNA solution 19. Two microliters of DNA solution 19, 3 µl of DNA solution 10 (described in EXAMPLE 22-(ii)) and 5µl of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent E. coli DH5 α cells were transformed with 45 5µl of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-CL. Mutagenesis of OCIF cDNA to prepare OCIF-CC, OCIF-CDD2, OCIF-CDD1, OCIF-CCR4 and OCIF-CCR3 was performed by a one-step PCR.

PCR reactions for mutagenesis to prepare OCIF-CC, OCIF-CDD2, OCIF-CDD1, OCIF-CCR4 and OCIF-CCR3

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5	10X Ex Taq Buffer (Takara Shuzo)	10 µl
	2.5 mM solution of dNTPs	8 µl
	the plasmid vector containing the entire OCIF cDNA described in EXAMPLE 11 (8ng/ml)	2 µl
	sterile distilled water	73.5 µl
10	20 µM solution of primer OCIF Xho F	5 µl
	100 µM solution of primer (for mutagenesis)	1 µl
	Ex Taq (Takara Shuzo)	0.5 µl

15

Table 12

mutants	primer-1	primer-2	primer-3	primer-4
OCIF-CL	IF 6	CL R	IF 14	CL F

Specific primers were used for each mutagenesis and other components were unchanged.

Primers used for the mutagenesis are shown in Table 13. Their nucleotide sequences are shown in SEQUENCE NO:57-61.

The components of each PCR were mixed in a microcentrifuge tube and PCR was performed as follows.

The microcentrifuge tubes were treated for 3 minutes at 97 °C and then incubated sequentially, for 30 seconds at 95 °C, 30 seconds at 50 °C and 3 minutes at 70 °C. This three-step incubation procedure was repeated 25 times, and after that, the tubes were incubated for 5 minutes at 70 °C. An aliquot of the reaction mixture was removed from each tube and analyzed by an agarose gel electrophoresis to confirm the size of each product.

The size of the PCR products was confirmed on an agarose gel. Excess primers in the PCRs were removed using Amicon microcon (Amicon) after completion of the reaction. The DNA fragments were precipitated with ethanol, dried under vacuum and dissolved in 40 µl of sterile distilled water. The DNA fragment in each DNA solution was digested with restriction enzymes Xho I and Bam HI. After the reactions, DNA was precipitated with ethanol, dried under vacuum and dissolved in 20µl of sterile distilled water.

The solutions containing DNA fragment with the CC deletion, the CDD2 deletion, the CDD1 deletion, the CCR4 deletion and the CCR3 deletion were designated as CC DNA solution, CDD2 DNA solution, CDD1 DNA solution, CCR4 DNA solution and CC R3 DNA solution, respectively.

Table 13

mutants	primers for the mutagenesis
OCIF-CC	CC R
OCIF-CDD2	CDD2 R
OCIF-CDD1	CDD1 R
OCIF-CCR4	CCR4 R
OCIF-CCR3	CCR3 R

40

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(2) Construction of vectors for expressing the OCIF mutants

pSK-OCIF-CL was digested with restriction enzymes Bam HI and Xho I. The Bam HI-Xho I DNA fragment containing the entire coding sequence for OCIF-CL was isolatedand dissolved in 20 µl of sterile distilled water. This DNA solution was designated as CL DNA solution. One microliter of pCEP 4 DNA solution and 6 µl of either of CL DNA solution, CC DNA solution, CDD2 DNA solution, CDD1 DNA solution, CCR4 DNA solution or CCR3 DNA solution were independently mixed with 7 µl of ligation buffer I of DNA ligation kit ver. 2 and ligation reactions were carried out. Competent

E. coli DH5 α cells (100 μ l) were transformed with 7 μ l of each ligation mixture. Ampicillin-resistant transformants were screened for clones containing plasmids which have the desirable mutations in OCIF cDNA by analyzing the DNA structure. In each plasmid, OCIF cDNA fragment having a deletion were inserted between the recognition sites of Xho I and Bam HI of pCEP 4. The plasmids containing the cDNA encoding OCIF-CL, OCIF-CC, OCIF-CDD1, OCIF-CDD2, OCIF-CCR4 and OCIF-CCR3 were designated pCEP4-OCIF-CL, pCEP4-OCIF-CC, pCEP4-OCIF-CDD2, pCEP4-OCIF-CDD1, pCEP4-OCIF-CCR4 and pCEP4-OCIF-CCR3, respectively.

iv) Preparation of OCIF mutants with C-terminal truncation

10 (1) Introduction of C-terminal truncation to OCIF

A series of OCIF mutants with C-terminal truncation was prepared. OCIF mutant in which 10 residues of from Gln at 371 to Leu at 380 are replaced with 2 residues of Leu-Val was designated OCIF-CBst. OCIF mutant in which 83 residues of from Cys 298 to Leu 380 are replaced with 3 residues of Ser-Leu-Asp was designated OCIF-CSph. OCIF mutant in which 214 residues of from Asn 167 to Leu 380 are removed was designated OCIF-CBsp. OCIF mutant in which 319 residues of from Asp 62 to Leu 380 are replaced with 2 residues of Leu-Val was designated OCIF-CPst. Positions of the amino acid residues are shown in SEQUENCE NO: 4.

Two micrograms each of pSK + -OCIF was digested with one of the restriction enzymes, Bst PI, Sph I, PstI (Takara Shuzo), and Bsp EI (New England Biolabs), and followed by phenol extraction and ethanol precipitation. The precipitated DNA was dissolved in 10 μ l of sterile distilled water. Ends of the DNAs in 2 μ l of each solution were blunted using a DNA blunting kit in final volumes of 5 μ l. To the reaction mixtures, 1 μ g (1 μ l) of an Amber codon-containing Xba I linker (5'-CTAGTCTAGACTAG-3') and 6 μ l of ligation buffer I of DNA ligation kit ver. 2 were added.

After the ligation reactions, 6 μ l each of the reaction mixtures was used to transform E. coli DH5 α . Ampicillin-resistant transformants were screened for clones containing plasmids. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmids thus obtained were named pSK-OCIF-CBst, pSK-OCIF-CSph, pSK-OCIF-CBsp and pSK-OCIF-CPst, respectively.

(2) Construction of vectors for expressing the OCIF mutants

30 pSK-OCIF-CBst, pSK-OCIF-CSph, pSK-OCIF-CBsp and pSK-OCIF-CPst were digested with restriction enzymes Bam HI and Xho I. The 1.5 kb of DNA fragment containing entire coding sequence for each OCIF mutant was isolated and dissolved in 20 μ l of sterile distilled water. These DNA solutions that contain the Bam HI-Xhol fragment derived from pSK-OCIF-CBst, pSK-OCIF-CSph, pSK-OCIF-CBsp and pSK-OCIF-CPst were designated as CBst DNA solution, CSph DNA solution, CBsp DNA solution and CPst DNA solution, respectively. One microliter of pCEP 4 DNA solution (described in EXAMPLE 22-ii)) and 6 μ l of either CBst DNA solution, CSph DNA solution, CBsp DNA solution or CPst DNA solution were independently mixed with 7 μ l of ligation buffer I of DNA ligation kit ver. 2 and ligation reactions were carried out. Competent E. coli DH5 α cells (100 μ l) were transformed with 7 μ l of each ligation mixture. Ampicillin-resistant transformants were screened for clones containing plasmids in which cDNA fragment is inserted between the recognition sites of Bam HI and Xho I of pCEP 4 by analyzing the DNA structure. The plasmids containing the cDNA encoding OCIF-CBst, OCIF-CSph, OCIF-CBsp and OCIF-CPst were designated as pCEP4-OCIF-CBst, pCEP4-OCIF-CSph, pCEP4-OCIF-CBsp and pCEP4-OCIF-CPst, respectively.

v) Preparation of vectors for expressing the OCIF mutants

45 E. coli clones harboring the expression vectors for OCIF mutants (total of 21 clones) were grown and the vectors were purified by QIAGEN column (QIAGEN). All the expression vectors were precipitated with ethanol and dissolved in appropriate volumes of sterile distilled water and used for further manipulations shown below.

vi) Transient expression of the cDNAs for OCIF mutants and biological activities of the mutants

50 OCIF mutants were produced using the expression vectors prepared in EXAMPLE 22-v). The method was essentially the same as described in EXAMPLE 13. Only the modified points are described below. A 24-well plate was used for the DNA transfection. 2X10⁵ cells of 293/EBNA suspended in IMDM containing 10% fetal bovine serum were seeded into each well of the plate. One microgram of purified vector DNA and 4 μ l of lipofectamine were used for each transfection. Mixture of an expression vector and lipofectamine in OPTI-MEM (GIBCO BRL) in a final volume of 0.5 ml was added to the cells in a well. After the cells were incubated at 37°C for 24 hr in a CO₂ incubator, the medium was replaced with 0.5 ml of Ex-cell 301 medium (JSR). The cells were incubated at 37 °C for 48 more hours in the CO₂ incubator. The conditioned medium was collected and used for assay for in vitro biological activity. The nucleotide

sequences of cDNAs for the OCIF mutants are shown in SEQUENCE NO:83-103. The deduced amino acid sequences for the OCIF mutants are shown in SEQUENCE NO: 62-82. The assay for in vitro biological activity was performed as described in EXAMPLE 13. Antigen concentration of each conditioned medium was determined by ELISA as described in EXAMPLE 24. Table 14 shows specific activity of the mutants relative to that of the unaltered OCIF.

5

Table 14

	mutants	activity
10	the unaltered OIF	++
	OCIF-C19S	+
	OCIF-C20S	±
	OCIF-C21S	±
15	OCIF-C22S	+
	OCIF-C23S	++
	OCIF-DCR1	±
20	OCIF-DCR2	±
	OCIF-DCR3	±
	OCIF-DCR4	±
25	OCIF-DDD1	+
	OCIF-DDD2	±
	OCIF-CL	++
	OCIF-CC	++
30	OCIF-CDD2	++
	OCIF-CDD1	+
	OCIF-CCR4	±
35	OCIF-CCR3	±
	OCIF-CBst	++
	OCIF-CSph	++
	OCIF-CBsp	±
40	OCIF-CPst	±
++ indicates relative activity more than 50% of that of the unaltered OCIF + indicates relative activity between 10% and 50% ± indicates relative activity less than 10%, or production level too low to determine the accurate biological activity		

45

vii) western blot analysis

Ten microliters of the final conditioned medium was used for western blot analysis. Ten microliters of the sample were mixed with 10 µl of SDS-PAGE sample buffer (0.5 M Tris-HCl, 20% glycerol, 4% SDS, 20µg/ml bromo phenol blue, 50 pH 6.8) boiled for 3 min. and subjected to a 10 % SDS polyacryl amide gel electrophoresis under non-reducing conditions. After the electrophoresis, the separated proteins were blotted to PVDF membrane (ProBlott^R, Perkin Elmer) using a semi-dry electroblotter (BIO-RAD). The membrane was incubated at 37°C with horseradish peroxidase labeled anti-OCIF antibodies for 2 hr. After the membrane was washed, protein bands which react with the labeled antibodies were detected using ECL system (Amersham). Two protein bands with approximate molecular masses of 60kD and 120kD were detected for the unaltered OCIF. On the other hand, almost exclusively 60kD protein band was detected for OCIF-C23S, OCIF-CL and OCIF CC. Protein bands with an approximate masses of 40kD-50kD and 30kD-40kD were the major ones for OCIF-CDD2 and OCIF-CDD1, respectively. These results indicate that Cys at 379 is responsible for the dimer formation, both the monomers and the dimers maintain the biological activity and a deletion of residues from Asp

at 177 to Leu at 380 does not abolish the biological activity of OCIF (positions of the amino acid resare shown in SEQUENCE NO: 4).

EXAMPLE 23

5

Isolation of human genomic OCIF gene

i) Screening of a human genomic library

An amplified human placenta genomic library in Lambda FIX II vector purchased from STRATAGENE was screened for the gene encoding human OCIF using the human OCIF cDNA as a probe. Essentially, screening was done according to the instruction manual supplied with the genomic library. The basic protocols described in Molecular Cloning: A Laboratory Manual also were employed to manipulate phage, E. coli, and DNA.

The library was titered, and 1×10^6 pfu of phage was mixed with XL1-Blue MRA host E. coli cells and plated on 20 plates (9 cm x 13 cm) with 9 ml per plate of top agarose. The plates were incubated overnight at 37°C. Filter plaque lifts were prepared using Hybond-N nylon membranes (Amersham). The membranes were processed by denaturation in a solution containing 1.5 M NaCl and 0.5 M NaOH for 1 minute at room temperature. The membranes were then neutralized by placing successively for one minute each in 1 M Tris-HCl (pH 7.5) and a solution containing 1.5 M NaCl and 0.5 M Tris-HCl (pH 7.5). The membranes were then transferred onto a filter paper wet with 2xSSC. Phage DNA was fixed on the membranes with 1200μJoules of UV energy in STRATALINKER UV crosslinker 2400 (STRATAGENE) and the membranes were air dried. The membranes were immersed in Rapid Hybridization buffer (Amersham) and incubated for one hour at 65 °C before hybridization with 32 P-labeled cDNA probe in the same buffer overnight at 65°C. Screening probe was prepared by labeling the OCIF cDNA with 32 P using the Megaprime DNA labeling system (Amersham). Approximately, 5×10^5 cpm probe was used for each ml of hybridization buffer. After the hybridization, the membranes were rinsed in 2xSSC for five minutes at room temperature. The membranes were then washed four times, 20 minutes each time, in 0.5xSSC containing 0.1 % SDS at 65 °C. After the final wash, the membranes were dried and subjected to autoradiography at -80 °C with SUPER HR-H X-ray film (FUJI PFOTO FILM Co., Ltd.) and an intensifying screen. Upon examination of the autoradiograms, six positive signals were detected. Agar plugs were picked from the regions corresponded to these signals for phage purification. Each agar plug was soaked overnight in 0.5 ml of SM buffer containing 1% chloroform to extract phage. Each extract containing phage was diluted 1000 fold with SM buffer and an aliquot of 1 ml or 20 ml was mixed with host E. coli described above. The mixture was plated on agar plates with top agarose as described above. The plates were incubated overnight at 37 °C, and filter lifts were prepared, prehybridized, hybridized, washed and autoradiographed as described above. This process of phage purification was applied to all six positive signals initially detected on the autoradiograms and was repeated until all phage plaques on agar plates hybridize with the cDNA probe. After purification, agar plugs of each phage isolate were soaked in SM buffer containing 1% chloroform and stored at 4 °C. Six individual phage isolates were designated λOIF3, λOIF8, λOIF9, λOIF11, λOIF12 and λOIF17, respectively.

ii) Analysis of the genomic clones by restriction enzyme digestion and Southern blot hybridization

40

DNA was prepared from each phage isolate by the plate lysate method as described in Molecular Cloning: A Laboratory Manual. DNA prepared from each phage was digested with restriction enzymes and the fragments derived from the digestion were separated on agarose gels. The fragments were then transferred to nylon membranes and subjected to Southern blot hybridization using OCIF cDNA as a probe. The results of the analysis revealed that the six phage isolates are individual clones. Among these fragments derived from the restriction enzyme digestion, those fragments which hybridized with the OCIF cDNA probe were subcloned into plasmid vectors and subjected to the nucleotide sequence analysis as described below.

iii) Subcloning restriction fragments derived from genomic clones into plasmid vectors and determination of the nucleotide sequence.

λOIF8 DNA was digested with restriction enzymes EcoRI and NotI, and the DNA fragments derived these from were separated on a 0.7% agarose gel. The 5.8 kilobase pairs (kb) EcoRI/NotI fragment was extracted from the gel using QIAEX II Gel Extraction Kit (QIAGEN) according to the procedure recommended by the manufacturer. The 5.8 kb EcoRI/NotI fragment was ligated with pBluescript II SK+ vector (STRATAGENE) which had been linearized with restriction enzymes EcoRI and NotI, using Ready-To-Go T4 DNA Ligase (Pharmacia) according to the procedure recommended by the manufacturer. Competent DH5 α E. coli cells (Amersham) were transformed with the recombinant plasmid and transformants were selected on L-plates containing 50 μg/ml of ampicillin. A clone harboring the recom-

binant plasmid containing the 5.8 kb EcoRI/NotI fragment was isolated and this plasmid was termed pBSG8-5.8. pBSG8-5.8 was digested with HindIII and 0.9 kb of DNA fragment derived from this digestion was isolated in the same manner as described above. This 0.9 kb fragment was then cloned in pBluescript II SK- at the HindIII site as described above. This recombinant plasmid containing 0.9 kb HindIII fragment was denoted pBS8H0.9.

5 λOIF11 DNA was digested with EcoRI and 6 kb, 3.6 kb, 2.6 kb EcoRI fragments were isolated in the same manner as described above and cloned in pBluescript II SK+ vector at the EcoRI site as described above. These recombinant plasmids were termed pBSG11-6, pBSG11-3.6, and pBSG11-2.6, respectively. pBSG11-6 was digested with HindIII and the digest was applied on a 0.7 % agarose gel. Three fragments, 2.2 kb, 1.1 kb, and 1.05 kb in length, were extracted from the gel and cloned independently in pBluescript II SK- vector at the HindIII site in the same manner as 10 described above. These recombinant plasmids were termed pBS6H2.2, pBS6 H1.1 and pBS6H1.05, respectively.

15 The nucleotide sequence of the cloned genomic DNA was determined using ABI DyeDeoxy Terminator Cycle Sequencing Ready Reaction Kit (PERKIN ELMER) and 373A DNA Sequencing system (Applied Biosystems). Plasmids pBSG8-5.8, pBS8H0.9, pBSG11-6, pBSG11-3.6, pBSG11-2.6, pBS6H2.2, pBS6H1.1 and pBS6H1.05 were prepared according to the alkaline-SDS procedure as described in Molecular Cloning: A Laboratory Manual and used as 20 templates for the DNA sequence analysis. Nucleotide sequence of the human OCIF gene was presented in Sequence No 104 and Sequence No 105. The nucleotide sequence of the DNA, between exon 1 and exon 2 was not entirely determined. There is a stretch of approximately 17 kb of nucleotides between the sequences given in sequence No. 104 and sequence No. 105.

25 EXAMPLE 24

Quantitation of OCIF by EIA

i) Preparation of anti-OCIF antibody

25 Male JW rabbits (Kitayama LABES Co., LTD) weighing 2.5-3.0 kg were used for immunization for preparing antiserum. Three male JW rabbits (Kitayama LABES Co., LTD) weighing 2.5-3.0 kg were used for immunization. For immunization, emulsion was prepared by mixing an equal volume of rOCIF (200 µg/ml) and complete Freund's adjuvant (Difco, Cat. 0638-60-7). The rabbits were immunized subcutaneously six times at the interval of one week with 1 ml of emulsion 30 per injection. The rabbits were injected six times at the interval of seven days subcutaneously. Whole blood was obtained ten days after the final immunization and serum was separated. Antibody was purified from serum as follows. Antiserum was diluted two-fold with PBS. After adding ammonium sulfate at a final concentration of 40 w/v %, antiserum was allowed to stand at 4 °C for 1 hr.. Precipitate obtained by centrifugation at 8000 x g for 20 min. was dissolved in a small volume of PBS and was dialyzed against PBS. The resulting solution was loaded onto a Protein G-Sepharose column (Pharmacia). After washing with PBS, absorbed immunoglobulin G was eluted with 0.1 M glycine-HCL buffer (pH 3.0). Elutes were neutralized with 1.5 M Tris-HCL buffer (pH 8.7) immediately and were dialyzed against PBS. Protein concentration was determined by absorbance at 280nm (E^{1%} 13.5).

40 Horseradish peroxidase labeled antibody was prepared using ImmunoPure Maleimide Activated Horseradish Peroxidase Kit (Pierce, Cat. 31494). Briefly, one mg of IgG was incubated with 80 ug of N-succinimidyl-S-acetylthioacetate for 30 min. After deacetylation with 5 mg of hydroxylamine HCl, modified IgG was separated by polyacrylamide desalting column. Protein pool mixed with one mg of maleimide activated horseradish peroxidase was incubated at room temperature for 1 hr.

45 ii) Quantitation of OCIF by sandwich EIA

50 Microtiter plates (Nunc MaxiSorp Immunoplate) were coated with rabbit anti-OCIF IgG by incubating 0.2 µg in 100 µl of 50 mM sodium bicarbonate buffer pH 9.6 at 4°C overnight. After blocking the plates by incubating for 1 hour at 37°C with 300 µl of 25% BlockAce/PBS (Snow Brand Milk Products), 100µl of samples were incubated for 2 hours at room temperature. After washing the plates three times with PBST (PBS containing 0.05% Tween20), 100 µl of 1:10000 diluted horseradish peroxidase labeled anti-OCIF IgG was added and incubated for 2 hours at room temperture. The amount of OCIF was determined by incubation with 100 µl of a substrate solution (TMB, ScyTek Lab., Cat. TM4999) and measurement of the absorbance at 450 nm using an ImmunoReader (Nunc NJ2000). Purified recombinant OCIF was used as a standard protein and a typical standard curve was shown in Fig. 13.

EXAMPLE 25

Anti-OCIF monoclonal antibody

- 5 i) Preparation of hybridoma producing anti-OCIF monoclonal antibody.

OCIF was purified to homogeneity from culture medium of human fibroblasts, IMR-90 by the purification method described in Example 11. Purified OCIF was dissolved in PBS at a concentration of 10 µg/100 µl. BALB/c mice were immunized by administrating this solution intraperitoneally three times every two weeks. In the first and the second 10 immunizations, the emulsion composed of an equal volume of OCIF and Freund's complete adjuvant was administered. Three days after the final administration, the spleen was taken out, lymphocytes were isolated and fused with mouse myeloma p3x63-Ag8.653 cells according to the conventional method using polyethyleneglycol. Then the fused cells were cultured in HAT medium to select hybridoma. Subsequently, to check whether the selected hybridomas produce anti-OCIF antibody, anti-OCIF antibody in each culture medium of hybridomas was determined by solid phase ELISA which 15 was prepared by coating each well in 96-well immunoplates (Nunc) with 100µl of purified OCIF (10µg/ml in 0.1 M NaHCO₃) and by blocking each well with 50% BlockAce (Snow Brand Milk Products Co. Ltd.). The hybridoma clones secreting anti-OCIF antibody were established by cloning 3 - 5 times by limit dilution and by screening using the above solid phase ELISA. Among thus obtained hybridoma clones, several hybridoma clones with high production of anti-OCIF antibody were selected.

- 20 ii) Production of anti-OCIF monoclonal antibodies.

Each hybridoma clone secreting anti-OCIF antibody, which was obtained in EXAMPLE 25-i), was transplanted intraperitoneally to mice given Pristane (Aldrich) at a cell density of 1 × 10⁶ cells/mouse. The accumulated ascites was collected 25 10 - 14 days after the transplantation and the ascites containing anti-OCIF specific monoclonal antibody of the present invention was obtained. Purified antibodies were obtained by Affigel protein A Sepharose chromatography (BioRad) according to the manufacturer's manual. That is, the ascites was diluted with equal volume of a binding buffer (BioRad) and applied to protein A column. The column was washed with a sufficient volume of the binding buffer and eluted with an elution buffer (BioRad). After neutralizing, the obtained eluate was dialyzed in water and subsequently lyophilized. 30 The purity of the obtained antibody was analyzed by SDS/PAGE and a homogenous band with a molecular weight of about 150,000 was detected.

iii) Selection of monoclonal antibody having high affinity to OCIF

35 Each antibody obtained in EXAMPLE 25-ii) was dissolved in PBS and the concentration of protein in the solution was determined by the method of Lowry. Each antibody solution with the same concentration was prepared and then serially diluted with PBS. Monoclonal antibodies, which can recognize OCIF even at highly diluted solution, were selected by solid phase ELISA described in EXAMPLE 25-ii). Thus three monoclonal antibodies A1G5, E3H8 and D2F4 can be selected.

40 iv) Determination of class and subclass of antibodies

The class and subclass of the antibodies of the present invention obtained in EXAMPLE 25-iii) were analyzed using 45 an immunoglobulin class and subclass analysis kit (Amersham). The procedure was carried out according to the protocol disclosed in the directions. The results were shown in Table 15. The antibodies of the present invention, E3H8, A1G5 and D2F4 belong to IgG₁, IgG_{2a} and IgG_{2b}, respectively.

Table 15

Analysis of class and subclass of the antibodies in the present invention.							
Antibody	IgG ₁	IgG _{2a}	IgG _{2b}	IgG ₃	IgA	IgM	κ
A1G5	-	+	-	-	-	-	+
E3H8	+	-	-	-	-	-	+
D2F4	-	-	+	-	-	-	+

v) Determination of OCIF by ELISA

Three kinds of monoclonal antibodies, A1G5, E3H8 and D2F4, which were obtained in EXAMPLE 25-iv), were used as solid phase antibodies and enzyme-labeled antibodies, respectively. Sandwich ELISA was constructed by each combination of solid phase antibody and labeled antibody. The labeled antibody was prepared using Immuno Pure Maleimide Activated Horseradish Peroxidase Kit (Pierce, Cat. No. 31494). Each monoclonal antibody was dissolved in 0.1 M NaHCO₃ at a concentration of 10 µg/ml, and 100 µl of the solution was added to each well in 96-well immunoplates (Nunc, MaxiSorp Cat. No. 442404) followed by allowing to stand at room temperature overnight. Subsequently, each well in the plates was blocked with 50% Blockace (Snow Brand Milk Products, Co., Ltd.) at room temperature for 50 minutes, and then was washed three times with PBS containing 0.1% Tween 20 (washing buffer).

A series of concentrations of OCIF was prepared by diluting OCIF with 1st reaction buffer (0.2 M Tris-HCl bufer, pH 7.4, containing 40% Blockace and 0.1% Tween 20). Each well in 96-well immunoplates was filled with 100µl of the prepared OCIF solution with each concentration, allowed to stand at 37 °C for 3 hours, and subsequently washed three times with the washing buffer. For dilution of POD-labeled antibody, 2nd reaction buffer (0.1 M Tris-HCl buffer, pH 7.4, containing 25% Blockace and 0.1% Tween 20) was used. POD-labeled antibody was diluted 400-fold with 2nd reaction buffer, and 100 µl of the diluted solution was added to each well in the immunoplates. Each imunoplate was allowed to stand at 37 °CC for 2 hours, and subsequently washed three times with the washing buffer. After washing, 100 µl of a substrate solution (0.1 M citrate-phosphate buffer, pH 4. 5, containing 0.4 mg/ml of o-phenylenediamine HCl and 0.006% H₂O₂) was added to each well in the immunoplates and the immunoplates were incubated at 37°C for 15 min.

The enzyme reaction was terminated by adding 50 µl of 6 N H₂SO₄ to each well. The optical density of each well was determined at 492 nm using an immunoreader (ImmunoReader NJ 2000, Nunc).

Using three kinds of monoclonal antibody in the present invention, each combination of solid phase and POD-labeled antibodies leads to a accurate determination of OCIF. Each monoclonal antibody in the present invention was confirmed to recognize a different epitope of OCIF. A typical standard curve of OCIF using a combination of solid phase antibody, A1G5 and POD-labeled antibody, E3H8 was shown in Fig. 14.

vi) Determination of OCIF in human serum

Concentration of OCIF in five samples of normal human serum was determined using an EIA system described in EXAMPLE 25-v). The immunoplates were coated with A1G5 as described in EXAMPLE 25-v), and 50 µl of 1st. reaction buffer was added to each well in the immunoplates. Subsequently, 50µl of each human serum was added to each well in the immunoplates. The immnuoplates were incubated at 37°C for 3 hours and then washed three times with the washing buffer. After washing, each well in the immunoplates was filled with 100µl of POD-E3H8 antibody diluted 400-fold with 2nd. reaction buffer and incubated at 37°C for 2 hours. After washing the immunoplates three times with the washing buffer, 100 µl of the substrate solution described in EXAMPLE 25-v) was added to each well and incubated at 37°C for 15 min. The enzyme reaction was terminated by adding 50 µl of 6 N H₂SO₄ to each well in the immunoplates. The optical density of each well was determined at 492 nm using an immunoreader (ImmunoReader NJ 2000, Nunc). 1st. reaction buffer containing the known amount of OCIF was treated in the same way and a standard curve of OCIF as shown in fig. 2 was obtained. Using the standard curve of OCIF, the amount of OCIF in human serum sample was determined. The results were shown in Table 14.

Table 14

The amount of OCIF in normal human serum	
Serum Sample	OCIF Concentration (ng/ml)
1	5.0
2	2.0
3	1.0
4	3.0
5	1.5

EXAMPLE 26

Therapeutic effect on osteoporosis

5 (1) Method

Male Fischer rats, 6 weeks-old, were subjected to denervation of left forelimb. These rats were assigned to four groups(10 rats/group) and treated as follows ; group A, sham operated rats without administration ; group B, denervated rats with intravenous administration of vehicle ; group C, denervated rats administered OCIF intravenously at a dose of 5 µg/kg twice a day ; group D, denervated rats administered OCIF intravenously at a dose of 50 µg/kg twice a day. After denervation, OCIF was administered daily for 14 days. After 2 weeks treatment, the animals were sacrificed and their forelimbs were dissected. Thereafter bones were tested for mechanical strength.

15 (2) Results

Decrease of bone strength was observed in the animals of control groups as compared to those animals of the normal groups while bone strength was increase in the groups of animal received 50 mg of OCIF per kg body weight.

Industrial availability

The present invention provides both a novel protein which inhibits formation of osteoclasts and a efficient procedure to produce the protein. The protein of the present invention has an activity to inhibit formation of osteoclasts. The protein will be useful for the treatment of many diseases accompanying bone loss, such as osteoporosis, and as an antigen to be used for the immunological diagnosis of such diseases.

25 Referring to the deposited the microorganism

Name and Address of the Depositary Authority

30 Name: National Institute of Bioscience and Human-Technology Agency of Industrial Science and Technology Ministry of International Trade and Industry

Address: 1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki-ken 305, JAPAN

Deposited date: June 21, 1995

(It was transferred from Bikkoken No. P-14998, which was deposited on June 21, 1995.

35 Transferred date: October 25, 1995)

Acession Number: FERM BP-5267

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT:

(A) NAME: SNOW BRANDS MILK PRODUCTS CO., LTD.

(B) STREET:

10 (C) CITY:

(D) STATE:

(E) COUNTRY:

15 (F) POSTAL CODE (ZIP):

(G) TELEPHONE:

(H) TELEFAX:

20 (I) TELEX:

20 (ii) TITLE OF INVENTION: Novel proteins and methods for producing the
proteins

25 (iii) NUMBER OF SEQUENCES: 105

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER:

30 (C) OPERATING SYSTEM:

(D) SOFTWARE: Wordperfect windows

(V) CURRENT APPLICATION DATA:

35 (A) APPLICATION NUMBER: JP

(B) FILE REFERENCE:

(C) FILING DATE:

40

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55

(2) INFORMATION FOR SEQUENCE ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 6

(B) TYPE : amino acid

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : peptide (an internal amino acid sequence of the protein)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 1:

Xaa Tyr His Phe Pro Lys

1 5

(2) INFORMATION FOR SEQUENCE ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 14

(B) TYPE : amino acid

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : peptide (an internal amino acid sequence of the protein)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO:2:

Xaa Gln His Ser Xaa Gln Glu Gln Thr Phe Gln Leu Xaa Lys

1 5 10

(2) INFORMATION FOR SEQUENCE ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 12

(B) TYPE : amino acid

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : peptide (an internal amino acid sequence of the protein)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 3:

Xaa Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys

1 5 10

(2) INFORMATION FOR SEQUENCE ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 380

(B) TYPE : amino acid

(D) TOPOLOGY : linear

5 (ii) MOLECULE TYPE : protein (OCIF protein without signal peptide)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO:4:

	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	Glu	Glu	Thr	Ser
1				5					10					15	
	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	Tyr	Leu	Lys
10					20					25				30	
	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	Cys	Pro
15					35				40				45		
	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	Leu
					50				55				60		
20	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu
					65				70				75		
	Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg
					80				85				90		
25	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro
					95				100				105		
	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val
30					110				115				120		
	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser
					125				130				135		
35	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu
					140				145				150		
	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser
					155				160				165		
40	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu
					170				175				180		
	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr
					185				190				195		
45	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	Asn	Leu	Pro	Gly	Thr	Lys
					200				205				210		
	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Gln	His	Ser	Ser
50					215				220				225		
	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn
					230				235		-		240		

Lys Asp Gln Asp Ile Val Lys Ile Ile Gln Asp Ile Asp Leu
 5 245 250 255
 Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr
 10 260 265 270
 Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys
 15 275 280 285
 Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro
 20 290 295 300
 Ser Asp Gln Ile Leu Lys Leu Ser Leu Trp Arg Ile Lys Asn
 25 305 310 315
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His
 30 320 325 330
 Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys
 35 335 340 345
 Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr
 40 350 355 360
 Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val
 45 365 370 375
 Lys Ile Ser Cys Leu
 50 380

(2) INFORMATION FOR SEQUENCE ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 401

(B) TYPE : amino acid

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF protein with signal peptide)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 5:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 40 -20 -15 -10
 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 45 -5 -1 1 5
 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 50 10 15 20
 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 25 25 30 35
 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His

	40	45	50
5	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu		
	55	60	65
	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys		
10	70	75	80
	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys		
	85	90	95
	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr		
15	100	105	110
	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe		
	115	120	125
	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn		
20	130	135	140
	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr		
	145	150	155
	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys		
25	160	165	170
	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala		
	175	180	185
30	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp		
	190	195	200
	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile		
	205	210	215
35	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys		
	220	225	230
	Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile		
40	235	240	245
	Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile		
	250	255	260
	Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu		
45	265	270	275
	Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr		
	280	285	290
50	Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser		
	295	300	305
	Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu		

310	315	320
		Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr
5	325	330 335
		Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe
10	340	345 350
		Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly
15	355	360 365
		Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
	370	375 380

(2) INFORMATION FOR SEQUENCE ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 1206
- (B) TYPE :: nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 6:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCCTCTGG TACCTACCTA AAACAACACT GTACAGCAA GTGGAAGACC 180
 GTGTGCGCCC CTIGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT 240
 30 CTATACTGCA GCCCCGTGTC CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420
 35 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT 480
 AGAAAACACA CAAATTGCGAG TGTCTTGTT CTCCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC 600
 CTGTGTGAGG AGGCATTCTT CAGGTTGCT GTTCCCTACAA AGTTTACGCC TAACTGGCTT 660
 40 AGTGTCTTGG TAGACAATTG GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 AACCGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840
 45 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAA 960
 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020

5 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAAACT 1080
 GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG 1140
 TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAAGGTCC AATCAGTAAA AATAAGCTGC 1200
 TTATAA 1206

10 (2) INFORMATION FOR SEQUENCE ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 15
- (B) TYPE : amino acid
- (D) TOPOLOGY : linear

15 (ii) MOLECULE TYPE : peptide (a N-terminal amino acid sequence of the protein)

20 (xi) SEQUENCE DESCRIPTION :SEQ ID NO:7:

Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser

1	5	10	15
---	---	----	----

25 (2) INFORMATION FOR SEQUENCE NO ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 1185
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

30 (ii) MOLECULE TYPE : cDNA (OCIF2)

35 (xi) SEQUENCE DESCRIPTION :SEQ ID NO:8

ATGAAACAAT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 40 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGTGC AATCGCACCC ACAACCCGCGT GTGCGAATGC 300
 AAGGAAGGGC GCTACCTTGA GATAGAGTTC TGCTTGAAAC ATAGGAGCTG CCCTCCTGGA 360
 TTTGGAGTGG TGCAAGCTGG AACCCCGAG CGAAATACAG TTTGCAAAAG ATGTCCAGAT 420
 45 GGGTTCTTCT CAAATGAGAC GTCATCTAAA GCACCCGTGA GAAAACACAC AAATTGCAGT 480
 GTCTTGGTC TCCTGCTAAC TCAGAAAGGA AATGCAACAC ACGACAACAT ATGTTCCGGA 540
 AACAGTGAAT CAACTCAAAA ATGTGGAATA GATGTTACCC TGTGTGAGGA GGCATTCTTC 600
 50 AGGTTTGCTG TTCCTACAAA GTTACGCTT AACTGGCTTA GTGTCTGGT AGACAATTG 660
 CCTGGCACCA AAGTAAACGC AGAGAGTGTGAGAGGATAA AACGGCAACA CAGCTCACAA 720

GAACAGACTT TCCAGCTGCT GAAGTTATGG AAACATCAAAC ACAAGACCA AGATATAAGTC 780
 5 AAGAAGATCA TCCAAGATAT TGACCTCTGT GAAAACAGCG TGCAAGCGGCAT CATTGGACAT 840
 GCTAACCTCA CCTTCGAGCA GCTTCGTAGC TTGATGGAAA GCTTACCGGG AAAGAAAGTG 900
 GGAGCAGAAG ACATTGAAAA AACAAATAAAG GCATGCAAAC CCAGTGACCA GATCCTGAAG 960
 CTGCTCAGTT TGTGGCGAAT AAAAATGGC GACCAAGACA CCTTGAGGG CCTAATGCAC 1020
 10 GCACTAAAGC ACTCAAAGAC GTACCACCTT CCCAAACTG TCACTCAGAG TCTAAAGAAG 1080
 ACCATCAGGT TCCTTCACAG CTTCAACAATG TACAAATTGT ATCAGAAGTT ATTTTTAGAA 1140
 ATGATAGGTA ACCAGGTCCA ATCAGTAAAA ATAAGCTGCT TATAA 1185

15 (2) INFORMATION FOR SEQUENCE ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 394

(B) TYPE : amino acid

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser		
-20	-15	-10
Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His		
-5	-1 1	5
Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro		
10	15	20
Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr		
25	30	35
Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His		
40	45	50
Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Cys		
55	60	65
Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr		
70	75	80
Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly		
85	90	95
Phe Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys		
100	105	110
Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys		
115	120	125

	Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu	
130	135	140
5	Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly	
145	150	155
	Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys	
160	165	170
10	Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro	
175	180	185
	Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val	
190	195	200
15	Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln	
205	210	215
20	Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys	
220	225	230
	Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys	
235	240	245
25	Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe	
250	255	260
	Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val	
265	270	275
30	Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser	
280	285	290
	Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly	
35	295	300
	Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser	
310	315	320
40	Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys	
325	330	335
	Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln	
340	345	350
45	Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys	
355	360	365
	Ile Ser Cys Leu	
50	370	373

(2) INFORMATION FOR SEQUENCE ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH : 1089
 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear

10 (ii) MOLECULE TYPE : cDNA (OCIF3)

(xi) SEQUENCE DESCRIPTION ID NO: 10:

ATGAACAAAGT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCCTCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTCGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCCTGT	480
AGAAAACACA	CAAATTGCGAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTCCCTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTCTTGG	TAGACAATT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	AGTTTGCGC	GAATAAAAAA	TGGCGACCAA	900
GACACCTTGA	AGGGCCTAAT	GCACCCACTA	AAGCACTCAA	AGACGTACCA	CTTTCCCAA	960
ACTGTCACTC	AGAGTCTAAA	GAAGACCATC	AGGTTCTTC	ACAGCTTCAC	AATGTACAAA	1020
TTGTATCAGA	AGTTATTTT	AGAAATGATA	GGTAACCAGG	TCCAATCAGT	AAAAATAAGC	1080
					TGCTTATAA	1089

40 (2) INFORMATION FOR SEQUENCE ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH : 362
 (B) TYPE : amino acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF3)

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser

	-20	-15	-10
	Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His		
5	-5	-1	5
	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro		
	10	15	20
	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr		
10	25	30	35
	Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His		
	40	45	50
15	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu		
	55	60	65
	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys		
20	70	75	80
	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys		
	85	90	95
	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr		
25	100	105	110
	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe		
	115	120	125
	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn		
30	130	135	140
	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr		
	145	150	155
35	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys		
	160	165	170
	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala		
40	175	180	185
	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp		
	190	195	200
	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile		
45	205	210	215
	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys		
	220	225	230
50	Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile		
	235	240	245
	Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile		

	250	255	260
5	Gly His Ala Asn Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln		
	265	270	275
10	Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr		
	280	285	290
15	Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile		
	295	300	305
20	Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu		
	310	315	320
25	Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser		
	325	330	335
30	Cys Leu		
	340 341		

(2) INFORMATION FOR SEQUENCE ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 465
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF4)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 12:

ATGAAACAAGT TGCTGTGCTG CTCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
35 CAGGAAACGT TTCCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCCTCCTGG TACCTACCTA AAACAAACACT GTACAGCAAA GTGGAAGACC	180
40 GTGTGCGGCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCAACCCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTGAAA	360
45 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GTACGTGTCA ATGTGCAGCA	420
AAATTAATTA GGATCATGCA AAGTCAGATA GTTGTGACAG TTTAG	465

(2) INFORMATION FOR SEQUENCE ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH :154
- (B) TYPE : amino acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

5 (ii) MOLECULE TYPE : protein (OCIF4)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

	Met Asn Lys Leu Leu Cys Cys Ser Leu Val Phe Leu Asp Ile Ser			
10	-20	-15	-0	
	Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His			
	-5	-1	1	5
15	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro			
	10	15	20	
	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr			
	25	30	35	
20	Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Asp Ser Trp His			
	40	45	50	
	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu			
	55	60	65	
25	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys			
	70	75	80	
	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys			
30	85	90	95	
	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr			
	100	105	110	
	Cys Gln Cys Ala Ala Lys Leu Ile Arg Ile Met Gln Ser Gln Ile			
35	115	120	125	
	Val Val Thr Val			
	130	133		

40 (2) INFORMATION FOR SEQUENCE ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 438

45 (B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF5)

50 (xi) SEQUENCE DESCRIPTION ID NO: 14:

ATGAACAAAGT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60

CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 5 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 10 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GATGCAGGAG AAGACCCAAG 420
 CCACAGATAT GTATCTGA 438

(2) INFORMATION FOR SEQUENCE ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 140
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF5)

(xi) SEQUENCE DESCRIPTION: ID NO: 15:

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 25 -20 -15 -10
 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 30 -5 -1 1 5
 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 35 10 15 20
 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 40 25 30 35
 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Asp Ser Trp His
 45 40 45 50
 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
 50 55 60 65
 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
 55 70 75 80
 45 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
 85 85 90 95
 His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Cys
 100 100 105 110
 50 Arg Arg Arg Pro Lys Pro Gln Ile Cys Ile
 115 115 120 124

(2) INFORMATION FOR SEQUENCE ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH : 20
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

10 (ii) MOLECULE TYPE : synthetic DNA (primer T3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

AATTAAACCCT CACTAAAGGG

20

15

(2) INFORMATION FOR SEQUENCE ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH : 22
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

25 (ii) MOLECULE TYPE : synthetic DNA (primer T7)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GTAATACGAC TCACTATAGG GC

22

30

(2) INFORMATION FOR SEQUENCE ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH : 20
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

40 (ii) MOLECULE TYPE : synthetic DNA (primer IF1)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 18:

ACATCAAAAC AAAGACCAAG

20

45

(2) INFORMATION FOR SEQUENCE ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH : 20
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

55

5 (ii) MOLECULE TYPE : synthetic DNA (primer IF2)
(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 19:
TCTTGGTCTT TGTGTTGATG

10 (2) INFORMATION FOR SEQUENCE ID NO: 20:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH : 20
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear
(ii) MOLECULE TYPE : synthetic DNA (primer IF3)
(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 20:
TTATTCGCCA CAAACTGAGC

15 (2) INFORMATION FOR SEQUENCE ID NO: 21:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH : 20
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear
(ii) MOLECULE TYPE : synthetic DNA (primer IF4)

20 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 21:
TTGTGAAGCT GTGAAGGAAAC

25 (2) INFORMATION FOR SEQUENCE ID NO: 22:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH : 20
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear
(ii) MOLECULE TYPE : synthetic DNA (primer IF5)

30 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 22:
GCTCAGTTG TGGCGAATAA

35 (2) INFORMATION FOR SEQUENCE ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 20
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF6)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 23:

GTGGGAGCGAG AAGACATTGA

20

(2) INFORMATION FOR SEQUENCE ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 20
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF7)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 24:

AATGAACAAC TTGCTGTGCT

20

(2) INFORMATION FOR SEQUENCE ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 20
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF8)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 25:

TGACAAATGT CCTCCTGGTA

20

(2) INFORMATION FOR SEQUENCE ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 20
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF9)

55

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 26:

AGGTAGGTAC CAGGAGGACA

20

5

(2) INFORMATION FOR SEQUENCE ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH : 20

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

15

(ii) MOLECULE TYPE : synthetic DNA (primer IF10)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 27:

GAGCTGCCCT CCTGGATTG

20

20

(2) INFORMATION FOR SEQUENCE ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH : 20

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

30

(ii) MOLECULE TYPE : synthetic DNA (primer IF11)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 28:

CAAACGTAT TTTCGCTCTGG

20

35

(2) INFORMATION FOR SEQUENCE ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH : 20

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

45

(ii) MOLECULE TYPE : synthetic DNA (primer IF12)

45

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 29:

GTGTGAGGAG GCATTCTTCA

20

50

(2) INFORMATION FOR SEQUENCE ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 32

55

- 5 (B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

10 (ii) MOLECULE TYPE : synthetic DNA (primer C19SF)
(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 30:
GAATCAACTC AAAAAAGTGG AATAGATGTT AC 32

15 (2) INFORMATION FOR SEQUENCE ID NO: 31:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH : 32
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

20 (ii) MOLECULE TYPE : synthetic DNA (primer C19SR)
(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 31:
GTAACATCTA TTCCACTTTT TTGAGTTGAT TC 32

25 (2) INFORMATION FOR SEQUENCE ID NO: 32:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH : 30
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

30 (ii) MOLECULE TYPE : synthetic DNA (primer C20SF)
(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 32:
ATAGATGTTA CCCTGAGTGA GGAGGCATTC 30

35 (2) INFORMATION FOR SEQUENCE ID NO: 33:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH : 30
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

40 (ii) MOLECULE TYPE : synthetic DNA (primer C20SR)
(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 33:

	GAATGCCTCC TCACTCAGGG TAACATCTAT	30
5	(2) INFORMATION FOR SEQUENCE ID NO: 34:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH : 31	
	(B) TYPE : nucleic acid	
	(C) STRANDEDNESS : single	
	(D) TOPOLOGY : linear	
15	(ii) MOLECULE TYPE : synthetic DNA (primer C21SF)	
	(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 34:	
	CAAGATATTG ACCTCAGTGA AACACAGCGTG C	31
20	(2) INFORMATION FOR SEQUENCE ID NO: 35:	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH : 31	
	(B) TYPE : nucleic acid	
	(C) STRANDEDNESS : single	
	(D) TOPOLOGY : linear	
30	(ii) MOLECULE TYPE : synthetic DNA (primer C21SR)	
	(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 35:	
	GCACCGCTGTT TTCACTGAGG GCAATATCTT G	31
35	(2) INFORMATION FOR SEQUENCE ID NO: 36:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH : 31	
	(B) TYPE : nucleic acid	
	(C) STRANDEDNESS : single	
	(D) TOPOLOGY : linear	
45	(ii) MOLECULE TYPE : synthetic DNA (primer C22SF)	
	(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 36:	
	AAAACAATAA AGGCAAGCAA ACCCAGTGAC C	31
50	(2) INFORMATION FOR SEQUENCE ID NO: 37:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH : 31	
	(B) TYPE : nucleic acid	

- (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear
- 5 (ii) MOLECULE TYPE : synthetic DNA (primer C22SR)
 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 37:
 GGTCACTGGG TTTGCTTGCC TTTATTGTTT T 31
- 10 (2) INFORMATION FOR SEQUENCE ID NO: 38:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH : 31
 15 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear
- 20 (ii) MOLECULE TYPE : synthetic DNA (primer C23SF)
 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 38:
 TCAGTAAAAA TAAGCAGCTT ATAAC TG GCC A 31
- 25 (2) INFORMATION FOR SEQUENCE ID NO: 39:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH : 31
 30 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear
- 35 (ii) MOLECULE TYPE : synthetic DNA (primer C23SR)
 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 39:
 TGGCCAGTTA TAAGCTGCTT ATTTTACTG A 31
- 40 (2) INFORMATION FOR SEQUENCE ID NO: 40:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH : 22
 45 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear
- 50 (ii) MOLECULE TYPE : synthetic DNA (primer IF 14)
 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 40:
 TTGGGGTTTA TTGGAGGAGA TG 22

(2) INFORMATION FOR SEQUENCE ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH : 36
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

10 (ii) MOLECULE TYPE : synthetic DNA (primer DCR1F)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 41:

15 ACCACCCAGG AACCTTGCCC TGACCCTAC TACACA

36

(2) INFORMATION FOR SEQUENCE ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH : 36
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

25 (ii) MOLECULE TYPE : synthetic DNA (primer DCR1R)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 42:

30 GTCAGGGCAA GGTTCCCTGGG TGGTCCACTT AATGGA

36

(2) INFORMATION FOR SEQUENCE ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH : 36
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

40 (ii) MOLECULE TYPE : synthetic DNA (primer DCR2F)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 43:

45 ACCGTGTGCG CCGAATGCAA GGAAGGGCGC TACCTT

36

(2) INFORMATION FOR SEQUENCE ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH : 36
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer DCR2R)
 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 44:
 5 TTCCTTCAT TCGGCGCACA CGGTCTTCCA CTTTGC 36

(2) INFORMATION FOR SEQUENCE ID NO: 45:
 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH : 36
 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear
 15 (ii) MOLECULE TYPE : synthetic DNA (primer DCR3F)
 (xi) SEQUENCE DESCRIPTION : SEQ ID NO: 45:
 20 AACCGCGTGT GCAGATGTCC AGATGGGTTTC TTCTCA 36

(2) INFORMATION FOR SEQUENCE ID NO: 46:
 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH : 36
 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear
 30 (ii) MOLECULE TYPE : synthetic DNA (primer DCR3R)
 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 46:
 35 ATCTGGACAT CTGCACACGC GGTTGTGGGT GCGATT 36

(2) INFORMATION FOR SEQUENCE ID NO: 47:
 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH : 36
 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear
 45 (ii) MOLECULE TYPE : synthetic DNA (primer DCR4F)
 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 47:
 50 ACAGTTTGCA AATCCGGAAA CAGTGAATCA ACTCAA 36

(2) INFORMATION FOR SEQUENCE ID NO: 48:
 55 (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH : 36
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

10 (ii) MOLECULE TYPE : synthetic DNA (primer DCR4R)
(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 48:
ACTGTTCCG GATTTGCAA CTGTATTTCG CTCTGG 36

15 (2) INFORMATION FOR SEQUENCE ID NO: 49:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH : 36
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

20 (ii) MOLECULE TYPE : synthetic DNA (primer DDD1F)
(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 49:
AATGTGGAAT AGATATTGAC CTCTGTGAAA ACAGCG 36

25 (2) INFORMATION FOR SEQUENCE ID NO: 50:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH : 36
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

30 (ii) MOLECULE TYPE : synthetic DNA (primer DDD1R)
(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 50:
AGAGGTCAAT ATCTATTCCA CATTGGAG TTGATT 36

35 (2) INFORMATION FOR SEQUENCE ID NO: 51:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH : 36
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

40 (ii) MOLECULE TYPE : synthetic DNA (primer DDD2F)
(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 51:
AGAGGTCAAT ATCTATTCCA CATTGGAG TTGATT 36

45 (2) INFORMATION FOR SEQUENCE ID NO: 52:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH : 36
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

50 (ii) MOLECULE TYPE : synthetic DNA (primer DDD2R)
(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 52:

	AGATCATCCA AGACGCCTA AAGCACTCAA AGACGT	36
5	(2) INFORMATION FOR SEQUENCE ID NO: 52:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH : 36	
10	(B) TYPE : nucleic acid	
	(C) STRANDEDNESS : single	
	(D) TOPOLOGY : linear	
	(ii) MOLECULE TYPE : synthetic DNA (primer DDD2R)	
15	(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 52:	
	GCTTTAGTGC GTCTGGATG ATCTTCTTGA CTATAT	36
20	(2) INFORMATION FOR SEQUENCE ID NO: 53:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH : 29	
25	(B) TYPE : nucleic acid	
	(C) STRANDEDNESS : single	
	(D) TOPOLOGY : linear	
	(ii) MOLECULE TYPE : synthetic DNA (primer XhoI F)	
30	(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 53:	
	GGCTCGAGCG CCCAGCCGCC GCCTCCAAG	29
35	(2) INFORMATION FOR SEQUENCE ID NO: 54:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH : 20	
40	(B) TYPE : nucleic acid	
	(C) STRANDEDNESS : single	
	(D) TOPOLOGY : linear	
	(ii) MOLECULE TYPE : synthetic DNA (primer IF 16)	
	(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 54:	
45	TTTGAGTGCT TTAGTGCGTG	20
50	(2) INFORMATION FOR SEQUENCE ID NO: 55:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH : 30	
	(B) TYPE : nucleic acid	

(C) STRANDEDNESS : single
 (D) TOPOLOGY : linear
 5 (ii) MOLECULE TYPE : synthetic DNA (primer CL F)
 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 55:
 TCACTAAAAA TAAGCTAACT GGAAATGGCC 30

10 (2) INFORMATION FOR SEQUENCE ID NO: 56:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH : 30
 15 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear
 20 (ii) MOLECULE TYPE : synthetic DNA (primer CL R)
 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 56:
 GGCCATTTCG AGTTAGCTTA TTTTACTGA 30

25 (2) INFORMATION FOR SEQUENCE ID NO: 57:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH : 29
 30 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear
 (ii) MOLECULE TYPE : synthetic DNA (primer CC R)
 35 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 57:
 CCGGATCCTC AGTGCTTAG TGCGTGCAT 29

40 (2) INFORMATION FOR SEQUENCE ID NO: 58:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH : 29
 45 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear
 (ii) MOLECULE TYPE : synthetic DNA (primer CCD2 R)
 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 58:
 50 CCGGATCCTC ATTGGATGAT CTTCTTGAC 29

(2) INFORMATION FOR SEQUENCE ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH : 29
 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 10 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer CCD1 R)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 59:

CCGGATCCTC ATATTCCACA TTTTGAGT

29

15

(2) INFORMATION FOR SEQUENCE ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH : 29
 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer CCR4 R)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 60:

CCGGATCCTC ATTTGCAAAC TGTATTCG

29

30

(2) INFORMATION FOR SEQUENCE ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH : 29
 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer CCR3 R)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 61:

CCGGATCCTC ATTGCACAC GCGGTTGTG

29

45

(2) INFORMATION FOR SEQUENCE ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH : 401
 (B) TYPE : amino acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear

55

(ii) MOLECULE TYPE : Protein (OCIF-C19S)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 62:

5	Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser		
	-20	-15	-10
10	Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His		
	-5	-1	5
15	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro		
	10	15	20
20	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr		
	25	30	35
25	Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His		
	40	45	50
30	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu		
	55	60	65
35	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys		
	70	75	80
40	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys		
	85	90	95
45	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr		
	100	105	110
50	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe		
	115	120	125
55	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn		
	130	135	140
60	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr		
	145	150	155
65	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Ser		
	160	165	170
70	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala		
	175	180	185
75	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp		
	190	195	200
80	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile		
	205	210	215
85	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys		
	220	225	230

	Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile	
235	240	245
5	Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile	
250	255	260
	Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu	
10	265	270
	Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr	
	280	285
	Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Ser	
15	295	300
	Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu	
	310	315
20	Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr	
	325	330
	Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe	
	340	345
25	Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly	
	355	360
	Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu	
30	370	375
		380

(2) INFORMATION FOR SEQUENCE ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH : 401			
	(B) TYPE : amino acid			
	(C) STRANDEDNESS : single			
40	(D) TOPOLOGY : linear			
	(ii) MOLECULE TYPE : Protein (OCIF-C20S)			
	(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 63:			
	Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser			
45	-20	-15	-10	
	Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His			
	-5	-1	1	5
50	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro			
	10	15	20	
	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr			

	25	30	35
5	Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His		
	40	45	50
	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu		
	55	60	65
10	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys		
	70	75	80
	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys		
	85	90	95
15	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr		
	100	105	110
	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe		
20	115	120	125
	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn		
	130	135	140
	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr		
25	145	150	155
	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys		
	160	165	170
	Gly Ile Asp Val Thr Leu Ser Glu Glu Ala Phe Phe Arg Phe Ala		
30	175	180	185
	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp		
	190	195	200
35	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile		
	205	210	215
	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys		
	220	225	230
40	Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile		
	235	240	245
	Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile		
45	250	255	260
	Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu		
	265	270	275
	Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr		
50	280	285	290
	Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser		

295 5 10 15 20 25 30 35 40 45 50	300 310 315 325 330 335 340 345 355 360 365 370 375	305 320 325 330 335 340 345 350 355 360 365 370 380
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Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu
 Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr
 Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe
 Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly
 Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu

(2) INFORMATION FOR SEQUENCE ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 401
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-C21S)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 64:

30 35 40 45 50	Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser -20 -15 -10 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His -5 -1 1 5 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro 10 15 20 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr 25 30 35 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His 40 45 50 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu 55 60 65 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys 70 75 80 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys 85 90 95
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	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr	
5	100	105
	110	
	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe	
	115	120
	125	
	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn	
10	130	135
	140	
	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr	
	145	150
	155	
	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys	
15	160	165
	170	
	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala	
	175	180
	185	
20	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp	
	190	195
	200	
	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile	
	205	210
	215	
25	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys	
	220	225
	230	
	Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile	
	235	240
	245	
30	Ile Gln Asp Ile Asp Leu Ser Glu Asn Ser Val Gln Arg His Ile	
	250	255
	260	
	Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu	
35	265	270
	275	
	Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr	
	280	285
	290	
40	Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Ser	
	295	300
	305	
	Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu	
	310	315
	320	
45	Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr	
	325	330
	335	
	Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe	
	340	345
	350	
50	Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly	
	355	360
	365	

Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
 370 375 380

5

(2) INFORMATION FOR SEQUENCE ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH : 401
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-C22S)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 65:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser			
-20	-15	-10	
Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His			
-5	-1	1	5
Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro			
10	15	20	
Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr			
25	30	35	
Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His			
30	45	50	
Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu			
35	55	60	65
Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys			
40	70	75	80
Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys			
45	85	90	95
His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr			
50	100	105	110
Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe			
55	115	120	125
Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn			
60	130	135	140
Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr			
65	145	150	155
His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys			

55

	160	165	170
5	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala		
	175	180	185
	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp		
10	190	195	200
	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile		
	205	210	215
	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys		
15	220	225	230
	Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile		
	235	240	245
	Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile		
20	250	255	260
	Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu		
	265	270	275
	Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr		
25	280	285	290
	Ile Lys Ala Ser Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser		
	295	300	305
	Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu		
30	310	315	320
	Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr		
	325	330	335
35	Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe		
	340	345	350
	Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly		
40	355	360	365
	Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu		
	370	375	380

45 (2) INFORMATION FOR SEQUENCE ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 401
- (B) TYPE : amino acid
- 50 (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-C23S)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 66:

5	Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser		
	-20	-15	-10
10	Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His		
	-5	-1 1	5
15	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro		
	10	15	20
20	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr		
	25	30	35
25	Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Asp Ser Trp His		
	40	45	50
30	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu		
	55	60	65
35	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys		
	70	75	80
40	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys		
	85	90	95
45	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr		
	100	105	110
50	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe		
	115	120	125
55	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn		
	130	135	140
60	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr		
	145	150	155
65	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys		
	160	165	170
70	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala		
	175	180	185
75	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp		
	190	195	200
80	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile		
	205	210	215
85	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys		
	220	225	230

Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile
 235 240 245
 5 Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile
 250 255 260
 Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu
 10 265 270 275
 Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr
 280 285 290
 15 Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser
 295 300 305
 Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu
 310 315 320
 20 Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr
 325 330 335
 Val Thr Gln Ser Leu Lys Thr Ile Arg Phe Leu His Ser Phe
 340 345 350
 25 Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly
 355 360 365
 Asn Gln Val Gln Ser Val Lys Ile Ser Ser Leu
 30 370 375 380

(2) INFORMATION FOR SEQUENCE ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH : 360
 (B) TYPE : amino acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-DCR1)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 67:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 45 -20 -15 -10
 Ile Lys Trp Thr Thr Gln Glu Pro Cys Pro Asp His Tyr Tyr Thr
 -5 -1 1 5
 50 Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val
 10 15 20
 Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His

	25	30	35
5	Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu		
	40	45	50
	Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val		
	55	60	65
10	Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro		
	70	75	80
	Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg		
	85	90	95
15	Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys		
	100	105	110
	Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser		
20	115	120	125
	Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe		
	130	135	140
	Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser		
25	145	150	155
	Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser		
	160	165	170
	Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe		
30	175	180	185
	Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile		
	190	195	200
35	Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val		
	205	210	215
	Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg		
40	220	225	230
	Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp		
	235	240	245
	Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu		
45	250	255	260
	Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr		
	265	270	275
	Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His		
50	280	285	290
	Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe		

295 5 310 325	300 315 320 330	305 320 335
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Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu
 Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu

10 (2) INFORMATION FOR SEQUENCE ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 359
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

20 (ii) MOLECULE TYPE : Protein (OCIF-DCR2)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 68:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser -20	-15	-10
Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His -5	-1	5
Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro 10	15	20
Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr 25	30	35
Val Cys Ala Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe 40	45	50
Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln 55	60	65
Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp 70	75	80
Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys 85	90	95
His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly 100	105	110
Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr 115	120	125
Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe 130	135	140

	Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val		
5	145	150	155
	Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val		
	160	165	170
	Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln		
10	175	180	185
	Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val		
	190	195	200
	Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln		
15	205	210	215
	Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser		
	220	225	230
20	Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile		
	235	240	245
	Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys		
	250	255	260
25	Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu		
	265	270	275
	Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe		
30	280	285	290
	Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu		
	295	300	305
	His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu		
35	310	315	320
	Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu		
	325	330	335

40 (2) INFORMATION FOR SEQUENCE ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 363
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

45 (ii) MOLECULE TYPE : protein (OCIF-DCR3)

50 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 69:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser

	-20	-15	-10
5	Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His		
	-5	-1 1	5
10	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro		
	10	15	20
15	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr		
	25	30	35
20	Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His		
	40	45	50
25	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu		
	55	60	65
30	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys		
	70	75	80
35	Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala		
	85	90	95
40	Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu		
	100	105	110
45	Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn		
	115	120	125
50	Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu		
	130	135	140
55	Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn		
	145	150	155
60	Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn		
	160	165	170
65	Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu		
	175	180	185
70	Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp		
	190	195	200
75	Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu		
	205	210	215
80	Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu		
	220	225	230
85	Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly		
	235	240	245
90	Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp		

	250	255	260
5	Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp		
	265	270	275
	Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys		
	280	285	290
10	Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr		
	295	300	305
	Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys		
	310	315	320
15	Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile		
	325	330	335
	Ser Cys Leu		
20	340		

(2) INFORMATION FOR SEQUENCE ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 359
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF-DCR4)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 70:

	Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser		
35	-20	-15	-10
	Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His		
	-5	-1 1	5
40	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro		
	10	15	20
	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr		
	25	30	35
45	Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His		
	40	45	50
	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu		
	55	60	65
50	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys		
	70	75	80

	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Phe Cys Leu Lys	
85	90	95
5	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr	
100	105	110
10	Pro Glu Arg Asn Thr Val Cys Lys Ser Gly Asn Ser Glu Ser Thr	
115	120	125
10	Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe	
130	135	140
15	Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val	
145	150	155
15	Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val	
160	165	170
20	Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln	
175	180	185
20	Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val	
190	195	200
25	Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln	
205	210	215
25	Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser	
220	225	230
30	Leu Met Glu Ser Leu Pro Gly Lys Val Gly Ala Glu Asp Ile	
235	240	245
35	Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys	
250	255	260
35	Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu	
265	270	275
40	Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe	
280	285	290
40	Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu	
295	300	305
45	His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu	
310	315	320
45	Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu	
325	330	335
50		

(2) INFORMATION FOR SEQUENCE ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- 5
 (A) LENGTH : 326
 (B) TYPE : amino acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear

10 (ii) MOLECULE TYPE : protein (OCIF-DDD1)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 71:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser
-20														-10
Ile	Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His
-5														5
Tyr	Asp	Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro
10														20
Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr
25														35
Val	Cys	Ala	Pro	Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His
40														50
Thr	Ser	Asp	Glu	Cys	Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu
55														65
Gln	Tyr	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys
70														80
Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys
85														95
His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr
100														110
Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe
115														125
Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn
130														140
Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr
145														155
His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys
160														170
Gly	Ile	Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	Arg	His	Ile
175														185
Gly	His	Ala	Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu	Met	Glu

	190	195	200
5	Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr		
	205	210	215
	Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser		
	220	225	230
10	Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu		
	235	240	245
	Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr		
	250	255	260
15	Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe		
	265	270	275
	Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly		
20	280	285	290
	Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu		
	295	300	305

(2) INFORMATION FOR SEQUENCE ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327
- (B) TYPE: amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF-DDD2)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 72:

	Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser		
	-20	-15	-10
30	Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His		
	-5	-1 1	5
	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro		
	10	15	20
40	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr		
	25	30	35
	Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His		
50	40	45	50
	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu		
	55	60	65

	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys	
5	70	75
	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys	
	85	90
	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr	
10	100	105
	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe	
	115	120
	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn	
15	130	135
	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr	
	145	150
20	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys	
	160	165
	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala	
	175	180
25	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp	
	190	195
	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile	
30	205	210
	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys	
	220	225
	Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile	
35	235	240
	Ile Gln Asp Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys	
	250	255
40	Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser	
	265	270
	Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile	
	280	285
45	Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu	
	295	300
		305

(2) INFORMATION FOR SEQUENCE ID NO: 73:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH : 399

(B) TYPE : amino acid

(C) STRANDEDNESS : single

5 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF-CL)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 73:

10	Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser		
	-20	-15	-10
15	Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His		
	-5	-1	1
20	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro		
	10	15	20
25	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr		
	25	30	35
30	Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His		
	40	45	50
35	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu		
	55	60	65
40	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys		
	70	75	80
45	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys		
	85	90	95
50	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr		
	100	105	110
55	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe		
	115	120	125
60	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn		
	130	135	140
65	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr		
	145	150	155
70	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys		
	160	165	170
75	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala		
	175	180	185
80	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp		
	190	195	200
85	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile		

	205	210	215
5	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys		
	220	225	230
	Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile		
10	235	240	245
	Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile		
	250	255	260
	Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu		
15	265	270	275
	Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr		
	280	285	290
	Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser		
20	295	300	305
	Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu		
	310	315	320
	Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr		
25	325	330	335
	Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe		
	340	345	350
30	355	360	365
	Asn Gln Val Gln Ser Val Lys Ile Ser		
	370	375	

35

(2) INFORMATION FOR SEQUENCE ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 351
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

45 (ii) MOLECULE TYPE : protein (OCIF-CC)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 74:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser

-20 -15 -10

50 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His

-5 -1 1 5

55

Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 10 15 20
 5 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 25 30 35
 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
 10 40 45 50
 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
 55 60 65
 15 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
 70 75 80
 20 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
 85 90 95
 His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
 100 105 110
 25 Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe
 115 120 125
 Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
 130 135 140
 30 Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr
 145 150 155
 His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys
 160 165 170
 35 Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala
 175 180 185
 Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp
 190 195 200
 40 Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 205 210 215
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys
 220 225 230
 45 Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile
 235 240 245
 Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile
 250 255 260
 50 Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu
 265 270 275

Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr
 280 285 290
 5 Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser
 295 300 305
 Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu
 10 310 315 320
 Met His Ala Leu Lys His
 325 330

(2) INFORMATION FOR SEQUENCE ID NO: 75:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 272
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-CDD2)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 75:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 25 -20 -15 -10
 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 30 -5 -1 1 5
 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 35 10 15 20
 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 40 25 30 35
 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
 45 40 45 50
 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
 50 55 60 65
 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
 55 70 75 80
 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
 60 85 90 95
 His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
 65 100 105 110
 Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe
 70 115 120 125

Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
 130 135 140
 5 Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr
 145 150 155
 His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys
 10 160 165 170
 Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala
 175 180 185
 Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp
 15 190 195 200
 Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 205 210 215
 20 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys
 220 225 230
 Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile
 235 240 245
 25 Ile Gln
 250

30 (2) INFORMATION FOR SEQUENCE ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 197
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-CDD1)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 76:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 -20 -15 -10
 40 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 -5 -1 1 5
 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 10 15 20
 45 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 25 30 35
 50 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Asp Ser Trp His

	40	45	50
	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu		
5	55	60	65
	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys		
	70	75	80
10	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys		
	85	90	95
	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr		
	100	105	110
15	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe		
	115	120	125
	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn		
20	130	135	140
	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr		
	145	150	155
25	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys		
	160	165	170
	Gly Ile		
	175		

30 (2) INFORMATION FOR SEQUENCE ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 143
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-CCR4)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 77:

	Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser		
	-20	-15	-10
45	Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His		
	-5	-1	1
	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro		
	10	15	20
50	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr		
	25	30	35

Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
 40 45 50
 5 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
 55 60 65
 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
 10 70 75 80
 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
 85 90 95
 His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
 15 100 105 110
 Pro Glu Arg Asn Thr Val Cys Lys
 115 120

20 (2) INFORMATION FOR SEQUENCE ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 106
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-CCR3)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 78:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 -20 -15 -10
 35 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 -5 -1 1 5
 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 10 15 20
 40 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 25 30 35
 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
 40 45 50
 45 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
 55 60 65
 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
 50 70 75 80
 Glu

85

5 (2) INFORMATION FOR SEQUENCE ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 393

(B) TYPE : amino acid

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-CBst)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 79:

15	Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser		
	-20	-15	-10
	Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His		
20	-5	-1	5
	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro		
	10	15	20
25	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr		
	25	30	35
	Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Asp Ser Trp His		
	40	45	50
30	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu		
	55	60	65
	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys		
	70	75	80
35	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys		
	85	90	95
	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr		
40	100	105	110
	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe		
	115	120	125
	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn		
45	130	135	140
	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr		
	145	150	155
	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys		
50	160	165	170
	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala		

55

	175	180	185
5	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp		
	190	195	200
	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile		
	205	210	215
10	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys		
	220	225	230
	Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile		
	235	240	245
15	Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile		
	250	255	260
	Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu		
20	265	270	275
	Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr		
	280	285	290
	Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser		
25	295	300	305
	Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu		
	310	315	320
30	Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr		
	325	330	335
	Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe		
	340	345	350
35	Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly		
	355	360	365
	Asn Leu Val		
40	370		

(2) INFORMATION FOR SEQUENCE ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH : 321

(B) TYPE : amino acid

(D) TOPOLOGY : linear

50 (ii) MOLECULE TYPE : Protein (OCIF-CSph)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 80:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser

	-20	-15	-10
	Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His		
5	-5	-1 1	5
	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro		
	10	15	20
10	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr		
	25	30	35
	Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His		
	40	45	50
15	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu		
	55	60	65
	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys		
20	70	75	80
	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys		
	85	90	95
	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr		
25	100	105	110
	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe		
	115	120	125
	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn		
30	130	135	140
	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr		
	145	150	155
35	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys		
	160	165	170
	Gly Ile Asp Val Thr Leu Cys Glu Ala Phe Phe Arg Phe Ala		
40	175	180	185
	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp		
	190	195	200
	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile		
45	205	210	215
	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys		
	220	225	230
50	Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile		
	235	240	245
	Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile		

250	255	260
	Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu	
265	270	275
	Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr	
280	285	290
	Ile Lys Ala Ser Leu Asp	
10 295	300	

(2) INFORMATION FOR SEQUENCE ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 202
- (B) TYPE : amino acid
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-CBsp)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 81:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser		
-20	-15	-10
Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His		
-5	-1 1	5
10	15	20
Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro		
25	30	35
Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr		
40	45	50
Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His		
55	60	65
Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu		
70	75	80
Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys		
85	90	95
Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys		
100	105	110
His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr		
115	120	125
Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe		
130	135	140

5
Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
145 150 155
Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr
160 165 170
His Asp Asn Ile Cys Ser Gly
10 175 180

(2) INFORMATION FOR SEQUENCE ID NO: 82:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 84
- (B) TYPE : amino acid
- (D) TOPOLOGY : linear

20 (ii) MOLECULE TYPE : Protein (OCIF-CPst)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 82:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
-20 -15 -10
Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
-5 -1 1 5
Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
30 10 15 20
Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
25 30 35
Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
35 40 45 50
Thr Ser Asp Glu Cys Leu Tyr Leu Val
55 60 63

(2) INFORMATION FOR SEQUENCE ID NO: 83:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 1206
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

50 (ii) MOLECULE TYPE : cDNA (OCIF-C19S)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 83:

5 ATGAAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCTTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGACACCCAG TGACGAGTGT 240
 CTATACTGCA GCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 10 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420
 GTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCGT 480
 15 AGAAAACACA CAAATTGCAG TGTCTTGCT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 CACGACAACA TATGTTCCGG AAACAGTGA TCAACTCAA AAAGTCCAAT AGATGTTACC 600
 20 CTGTGTGAGG AGGCATTCTT CAGGTTGCT GTTCCCTACAA AGTTTACGCC TAACTGGCTT 660
 AGTGTCTTGG TAGACAATT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 AACACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 25 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCAATGCAA 960
 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTTGGCAA TAAAAAATGG CGACCAAGAC 1020
 30 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCCAAACT 1080
 GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCCTCACA GCTTCACAAT GTACAAATTG 1140
 TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAAGTCC AATCAGTAAA AATAAGCTGC 1200
 TTATAA 1206

(2) INFORMATION FOR SEQUENCE ID NO: 84:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 1206
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- 40 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-C20S)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 84:

45 ATGAAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCTTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 50 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGACACCCAG TGACGAGTGT 240
 CTATACTGCA GCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300

CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 5 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420
 GTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT 480
 AGAAAACACA CAAATTGCAG TGTCTTGGT CTCTGCTAA CTCAGAAAGG AAATGCAACA 540
 10 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600
 CTGAGTGAGG AGGCATTCTT CAGGTTTGCT GTTCTACAA AGTTTACGCC TAATGGCTT 660
 AGTGTCTTGG TAGACAATT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 15 AACCGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 AACAAAGACC AAGATATACT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
 20 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCAATGCAA 960
 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAAATGG CGACCAAGAC 1020
 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCAACTT TCCCCAAACT 1080
 GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG 1140
 TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC 1200
 25 TTATAA 1206

(2) INFORMATION FOR SEQUENCE ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 1206
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-C21S)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 85:

40 ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCCAG TGACGAGTGT 240
 45 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420
 50 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT 480
 AGAAAACACA CAAATTGCAG TGTCTTGGT CTCTGCTAA CTCAGAAAGG AAATGCAACA 540
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600

CTGTGTGAGG AGGCATTCTT CAGGTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660
 5 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 AACCGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 10 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTAG TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
 15 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA^GGCATGCAA 960
 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAAATGG CGACCAAGAC 1020
 ACCTTGAAGG GCCTTAATGCA CGCACTAAAG CACTCAAAGA CGTACCAACTT TCCCAAAACT 1080
 GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG 1140
 TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAAGTCC AATCAGTAAA AATAAGCTGC 1200
 20 TTATAAA 1206

(2) INFORMATION FOR SEQUENCE ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 1206
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-C22S)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 86:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCTCTAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 35 TGTGACAAAT GTCTCTCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 40 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCGT 480
 AGAAAACACA CAAATTGCAG TGTCTTGGT CTCTGCTAA CTCAGAAAGG AAATGCAACA 540
 45 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC 600
 CTGTGTGAGG AGGCATTCTT CAGGTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660
 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 50 AACCGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900

AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCAACCAAA 960
 5 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020
 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAAACT 1080
 GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCCTTCACA GCTTCACAAT GTACAAATTG 1140
 TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAAGGTCC AATCAGTAAA AATAAGCTGC 1200
 10 TTATAA 1206

(2) INFORMATION FOR SEQUENCE ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH : 1206
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-C23S)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 87:

25 ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCCTCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 30 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420
 35 GTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT 480
 AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 CACCGACAACA TATGTTCCGG AAACAGTGA TCAACTCAA AATGTGGAAT AGATGTTACC 600
 40 CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660
 AGTGTCTTGG TAGACAATTG GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840
 45 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA 960
 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020
 50 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAAACT 1080
 GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCCTTCACA GCTTCACAAT GTACAAATTG 1140
 TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAAGGTCC AATCAGTAAA AATAAGCAGC 1200

TTATAA

1206

5 (2) INFORMATION FOR SEQUENCE ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 1083
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

10 (ii) MOLECULE TYPE : cDNA (OCIF-DCR1)

15 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 88:

ATGAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 20 CAGGAACCTT GCCCTGACCA CTACTACACA GACAGCTGGC ACACCAAGTGA CGAGTGTCTA 120
 TACTGCAGCC CCGTGTGCAA GGAGCTGCAG TACGTCAAGC AGGAGTGCAA TCGCACCCAC 180
 AACCGCGTGT GCGAATGCAA GGAAGGGCGC TACCTTGAGA TAGAGTTCTG CTTGAAACAT 240
 25 AGGAGCTGCC CTCCCTGGATT TGGAGTGGTG CAAGCTGGAA CCCCAGAGCG AAATACAGTT 300
 TGCAAAAGAT GTCCAGATGG GTTCTTCTCA AATGAGACGT CATCTAAAGC ACCCTGTAGA 360
 AAACACACAA ATTGCAGTGT CTTTGGTCTC CTGCTAACTC AGAAAGGAAA TGCAACACAC 420
 GACAACATAT GTTCCGGAAA CAGTGAATCA ACTCAAAAAT GTGGAATAGA TGTTACCTG 480
 30 TGTGAGGAGG CATTCTTCAG GTTTGCTGT CCTACAAAGT TTACGCCAA CTGGCTTAGT 540
 GTCTTGGTAG ACAATTTGCC TGGCACCAAA GTAAACGCAG AGAGTGTAGA GAGGATAAAA 600
 CGGCAACACA GCTCACAAGA ACAGACTTTC CAGCTGCTGA AGTTATGGAA ACATCAAAAC 660
 AAAGACCAAG ATATAGTCAA GAAGATCATC CAAGATATTG ACCTCTGTGA AACAGCGTG 720
 35 CAGCGGCACA TTGGACATGC TAACCTCACCC TTGAGCAGC TTGCTAGCTT GATGGAAAGC 780
 TTACCGGGAA AGAAAGTGGG AGCAGAACAC ATTGAAAAAA CAATAAAGGC ATGCAAAACCC 840
 AGTGACCAGA TCCTGAAGCT GCTCAGTTG TGGGAATAA AAAATGGCGA CCAAGACACC 900
 40 TTGAAGGGCC TAATGCACGC ACTAAAGCAC TCAAAGACGT ACCACTTCC CAAAAGTGTG 960
 ACTCAGAGTC TAAAGAAGAC CATCAGGTTG CTTCACAGCT TCACAATGTA CAAATTGTAT 1020
 CAGAAGTTAT TTTAGAAAT GATAGGTAAC CAGGTCCAAT CAGTAAAAAT AAGCTGCTTA 1080
 TAA 1083

45 (2) INFORMATION FOR SEQUENCE ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 1080
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-DCR2)

5 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 89:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCTTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 10 TGTGACAAAT GTCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCG AATGCAAGGA AGGGCGCTAC CTTGAGATAG AGTTCTGCTT GAAACATAGG 240
 AGCTGCCCTC CTGGATTGG AGTGGTGCAA GCTGGAACCC CAGAGCGAAA TACAGTTGC 300
 15 AAAAGATGTC CAGATGGTTT CTTCTCAAAT GAGACGTAT CTAAGCACC CTGTAGAAAA 360
 CACACAAATT GCAGTGTCTT TGGTCTCCTG CTAACTCAGA AAGGAAATGC AACACACGAC 420
 AACATATGTT CGGGAAACAG TGAATCAACT CAAAAATCTG GAATAGATGT TACCTGTGT 480
 20 GAGGAGGCAT TCTTCAGGTT TGCTGTTCTT ACAAAAGTTA CGCCTAACTG GCTTAGTGTC 540
 TTGGTAGACA ATTTGCCTGG CACCAAAGTA AACGCAGAGA GTGTAGAGAG GATAAACCGG 600
 CAACACAGCT CACAAGAACCA GACTTCCAG CTGCTGAAGT TATGAAACA TCAAAACAAA 660
 GACCAAGATA TAGTCAAGAA GATCATCCAA GATATTGACC TCTGTAAAA CAGCGTGCAG 720
 25 CGGCACATTG GACATGCTAA CCTCACCTTC GAGCAGCTTC GTAGCTTGAT GGAAAGCTTA 780
 CCGGGAAAGA AAGTGGGAGC AGAAGACATT GAAAAAAACAA TAAAGGCATG CAAACCCAGT 840
 GACCAGATCC TGAAGCTGCT CAGTTGTGG CGAATAAAAAA ATGGCGACCA AGACACCTTG 900
 30 AAGGGCCTAA TGCACGCCTA AAAGCACTCA AAAGACGTACC ACTTICCAA AACTGTCACT 960
 CAGAGTCTAA AGAAGACCAT CAGGTTCCCTT CACAGCTTCA CAATGTACAA ATTGTATCAG 1020
 AAGTTATTTT TAGAAATGAT AGGTAACCAG GTCCAATCAG TAAAAATAAG CTGCTTATAA 1080

35 (2) INFORMATION FOR SEQUENCE ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 1092

40 (B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-DCR3)

45 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 90:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCTTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 50 TGTGACAAAT GTCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCG CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACCGAGTGT 240

CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 5 CACAACCGCG TGTGCAGATG TCCAGATGGG TTCTTCTCAA ATGAGACGTC ATCTAAAGCA 360
 CCCTGTAGAA AACACACAAA TTGCAGTGTG TTTGGTCTCC TGCTAACTCA GAAAGGAAAT 420
 10 GCAACACACG ACAACATATG TTCCGGAAAC AGTGAATCAA CTCAAAAATG TGGAATAGAT 480
 GTTACCCGTG GTGAGGAGGC ATTCTTCAGG TTTGCTGTTG CTACAAAGTT TACGCCAAC 540
 15 TGGCTTAGTG TCTTGGTAGA CAATTTGCCT GGCACCAAAG TAAACGCAGA GAGTGTAGAG 600
 AGGATAAAAC GGCAACACAG CTCACAAGAA CAGACTTCC AGCTGCTGAA GTTATGGAAA 660
 CATCAAACAA AAGACCAAGA TATAGTCAAG AAGATCATCC AAGATATTGA CCTCTGTGAA 720
 20 AACACGGTGC AGCGGCACAT TGGACATGCT AACCTCACCT TCGAGCAGCT TCGTAGCTTG 780
 ATGGAAAGCT TACCGGGAAA GAAAGTGGGA GCAGAAGACA TTGAAAAAAC AATAAAGGCA 840
 TGCAAACCCA GTGACCAGAT CCTGAAGCTG CTCAGTTGT GGCGAATAAA AAATGGCGAC 900
 25 CAAGACACCT TGAAGGGCCT AATGCACCGCA CTAAAGCACT CAAAGACGTA CCACCTTCCC 960
 AAAACTGTCA CTCAGAGTCT AAAGAAGACC ATCAGGTTCC TTCACAGCTT CACAATGTAC 1020
 AAATTGTATC AGAAGTTATT TTTAGAAATG ATAGGTAACC AGGTCCAATC AGTAAAAATA 1080
 AGCTGCTTAT AA 1092

25 (2) INFORMATION FOR SEQUENCE ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 1080
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

30 (ii) MOLECULE TYPE : cDNA (OCIF-DCR4)

35 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 91:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 40 CAGGAAACGT TTCCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 45 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420
 50 GTTTCCAAT CCCGAAACAG TGAATCAACT CAAAAATGTG GAATAGATGT TACCCGTGTT 480
 GAGGAGGCAT TCTTCAGGTT TGCTGTTCCCT ACAAAAGTTA CGCCTAACTG GCTTAGTGTC 540
 TTGGTAGACA ATTTGCCCTGG CACCAAAGTA AACGCAGAGA GTGTAGAGAG GATAAAACGG 600
 CAACACAGCT CACAAGAACAA GACTTTCCAG CTGCTGAAGT TATGGAAACA TCAAAACAAA 660

GACCAAGATA TAGTCAAGAA GATCATCCAA GATATTGACC TCTGTAAAAA CAGCGTGCAG 720
 CGGCACATTG GACATGCTAA CCTCACCTTC GAGCAGCTTC GTAGCTTGAT GGAAAGCTTA 780
 CCGGGAAAGA AAGTGGGAGC AGAAGACATT GAAAAAAACAA TAAAGGCATG CAAACCCAGT 840
 GACCAAGATCC TGAAGCTGCT CAGTTTGCGAATAAAAAA ATGGCGACCA AGACACCTTG 900
 AAGGGCCTAA TGACACGCACT AAAGCACTCA AAGACGTACC ACTTTCCCAA AACTGTCACT 960
 10 CAGAGTCTAA AGAAGACCAT CAGGTTCCCTT CACAGCTTCA CAATGTACAA ATTGTATCAG 1020
 AAGTTATTT TAGAAATGAT AGGTAACCAAG GTCCAATCAG TAAAAATAAG CTGCTTATAA 1080

(2) INFORMATION FOR SEQUENCE ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 981
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-DDD1)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 92:

25 ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 30 TGTGACAAAT GTCCCTCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACCGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 35 CATAGGAGCT GCCCTCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT 480
 AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 40 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATATTGAC 600
 CTCTGTGAAA ACAGCGTGCA GCGGCACATT GGACATGCTA ACCTCACCTT CGAGCAGCTT 660
 CGTAGCTTGA TGGAAAGCTT ACCGGGAAAG AAAGTGGGAG CAGAAGACAT TGAAAAAAACA 720
 ATAAAGGCAT GCAAACCCAG TGACCAAGATC CTGAAGCTGC TCAGTTGTG GCGAATAAAA 780
 45 AATGGCGACC AAGACACCTT GAAGGGCTA ATGCACGCAC TAAAGCACTC AAAGACGTAC 840
 CACTTTCCCA AAACTGTCAC TCAGAGTCTA AAGAAGACCA TCAGGTTCCCT TCACAGCTTC 900
 ACAATGTACA AATTGTATCA GAAGTTATTT TTAGAAATGA TAGGTAACCA GGTCCAATCA 960
 GTAAAAATAA GCTGCTTATAA A 981

(2) INFORMATION FOR SEQUENCE ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- 5
 (A) LENGTH : 984
 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear

10 (ii) MOLECULE TYPE : cDNA (OCIF-DDD2)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 93:

15	ATGAAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
	CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
20	TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAA GTGGAAGACC 180
	GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
25	CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
	CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
	CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTCCAAGCTG GAACCCCAGA GCGAAATACA 420
30	GTTTGCAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT 480
	AGAAAACACA CAAATTGCAAG TGTCTTTGGT CTCCCTGCTAA CTCAGAAAGG AAATGCAACA 540
	CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC 600
35	CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCCTACAA AGTTTACGCC TAACTGGCTT 660
	AGTGTCTTGG TAGACAATTG GCCTGGCACCC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
	AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
	AACAAAGACC AACATATAGT CAAGAAGATC ATCCAAGACG CACTAAAGCA CTCAAAGACG 840
	TACCACTTTC CCAAAACTGT CACTCAGAGT CTAAGAAGA CCATCAGGTT CCTTCACAGC 900
40	TTCACAATGT ACAAAATTGTA TCAGAAGTTA TTTTAGAAA TGATAGGTAA CCAGGTCCAA 960
	TCAGTAAAAA TAAGCTGCTT ATAA 984

(2) INFORMATION FOR SEQUENCE ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- 45
 (A) LENGTH : 1200
 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CL)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 94:

50	ATGAAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
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5 CAGGAAACGT TTCCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 10 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420
 GTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCGT 480
 AGAAAACACA CAAATTGCAAG TGTCTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 CACGACAACA TATGTTCCGG AAACAGTGA TCAACTCAA AATGTGGAAT AGATGTTACC 600
 15 CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAATGGCTT 660
 AGTGTCTTGG TAGACAATT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 AAACGGCAAC ACAGCTACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 20 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCAATGCAA 960
 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020
 25 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCCAAACT 1080
 GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCCTCACA GCTTCACAAT GTACAAATTG 1140
 TATCAGAAGT TATTTTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTAA 1200

30 (2) INFORMATION FOR SEQUENCE ID NO: 95:
 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 1056
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

35 (ii) MOLECULE TYPE : cDNA (OCIF-CC)

40 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 95:

45 ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 50 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420

5 GTTTCAAAA GATGTCAGA TGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT 480
AGAAAACACA CAAATTGCAG TGTCTTGCT CTCCGTCAA CTCAGAAAGG AAATGCAACA 540
CACCGACAACA TATGTTCCGG AACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC 600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCCTACAA AGTTTACGCC TAACTGGCTT 660
AGTGTCTTGG TAGACAATT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
AACAGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
10 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
AGCTTACCGG GAAAGAAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAA 960
15 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTGA 1056

(2) INFORMATION FOR SEQUENCE ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 819
 - (B) TYPE : nucleic acid
 - (C) STRANDEDNESS : single
 - (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CDD2)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 96:

ATGAAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTG 120
TGTGACAAAT GTCCCTCTGG TACCTACCTA AAACAAACACT GTACAGCAAA GTGGAAGACC 180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCAC 300
CACAACCGCG TGTGCGAACATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT 480
AGAAAACACA CAAATTGCAAG TGTCTTGGT CTCCCTGCTAA CTCAGAAAGG AAATGCAACA 540
CACGACAACA TATGTTCCGG AAACAGTGA TCAACTCAA AATGTGGAAT AGATGTTACC 600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCCTACAA AGTTTACGCC TAACTGGCTT 660
AGTGTCTTGG TAGACAATTG GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
AACCGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAATGA 819

(2) INFORMATION FOR SEQUENCE ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 594
 - (B) TYPE : nucleic acid
 - (C) STRANDEDNESS : single
 - (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CDD1)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 97:

ATGAAACAACCT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AACCTCTCA TCAGCTGTTG 120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
CACAAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCGTG 480
AGAAAAACACA CAAATTGCAG TGTCTTGGT CTCTGCTAA CTCAGAAAGG AAATGCAACA 540
CACGACAAACA TATGTTCCGG AAACAGTGAAC TCAACTCAA AATGTGGAAT ATGA. 594

(2) INFORMATION FOR SEQUENCE ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 432
 - (B) TYPE : nucleic acid
 - (C) STRANDEDNESS : single
 - (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CCR4)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 98:

ATGAAACAAC TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACCC 60
CAGGAAACGT TTCCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAAACACT GTACAGCAAA GTGGAAGACC 180
GTGTGCGGCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCCAG TGACGAGTGT 240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
CACAAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTGAAA 360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420
GTTTGCAAAT GA 432

(2) INFORMATION FOR SEQUENCE ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 321

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CCR3)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 99:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG A 321

(2) INFORMATION FOR SEQUENCE ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 1182

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CBst)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 100:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420
 GTTTGAAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCGT 480
 AGAAAACACA CAAATTGCAG TGTCTTGGT CTCTGCTAA CTCAGAAAGG AAATGCAACA 540
 CACGACAAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC 600
 CTGTGTGAGG AGGCATTCTT CAGGTTGCT GTTCTACAA AGTTTACGCC TAACTGGCTT 660

AGTGTCTTGG TAGACAATT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 5 AACCGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCAATGCAA 960
 10 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAAATGG CGACCAAGAC 1020
 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAAACT 1080
 GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCCTCACA GCTTCACAAT GTACAAATTG 1140
 TATCAGAACT TATTTTTAGA AATGATAGGT AACCTAGTCT AG 1182

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(2) INFORMATION FOR SEQUENCE ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 966
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CSph)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 101:

30 ATGAAACAAT TGCTGTGCTG CGCGCTCGTG TTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCCTCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 35 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420
 40 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT 480
 AGAAAACACA CAAATTGCGAG TGTCTTTGGT CTCTGCTAA CTCAGAAAGG AAATGCAACA 540
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC 600
 CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCCTACAA AGTTTACGCC TAACTGGCTT 660
 45 AGTGTCTTGG TAGACAATT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 AAACCGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
 50 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCTAGTCTA 960
 GACTAG 966

55

(2) INFORMATION FOR SEQUENCE ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 564
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CBsp)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 102:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCCGCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCGT 480
 AGAAAACACA CAAATTGCAG TGTCTTGTT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 CACGACAAACA TATGTTCCGG CTAG 564

(2) INFORMATION FOR SEQUENCE ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 255
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-Pst)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 103:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCCGCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT 240
 CTATAACCTAG TCTAG 255

(2) INFORMATION FOR SEQUENCE ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH : 1317
 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : double
 10 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : human OCIF genomic DNA-1

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 104:

15	CTGGAGACAT ATAACTTGAA CACTTGGCCC TGATGGGAA GCAGCTCTGC AGGGACTTT	60
	TCAGCCATCT GTAAACAATT TCAGTGGCAA CCCCGGAACGT GTAATCCATG AATGGGACCA	120
	CACTTACAA GTCATCAAGT CTAACCTCTA GACCAGGGAA TTAATGGGG AGACAGCGAA	180
20	CCCTAGAGCA AAGTGCCAAA CTTCTGTCGA TAGCTTGAGG CTAGTGGAAA GACCTCGAGG	240
	AGGCTACTCC AGAACGTTCAAG CGCGTAGGAA GCTCCGATAAC CAATAGCCCT TTGATGATGG	300
	TGGGGTTGGT GAAGGGAACA GTGCTCCGCA AGGTTATCCC TGCCCCAGGC AGTCCAATT	360
25	TCACTCTGCA GATTCTCTCT GGCTCTAACT ACCCCAGATA ACAAGGAGTG AATGCAGAAT	420
	AGCACGGGCT TTAGGGCCAA TCAGACATTA GTTAGAAAAA TTCTACTAC ATGGTTTATG	480
	TAAACTTGAA GATGAATGAT TGCGAACTCC CCGAAAAGGG CTCAGACAAT GCCATGCATA	540
	AAGAGGGGCC CTGTAATTG AGGTTTCAGA ACCCGAAGTG AAGGGTCAG GCAGCCGGT	600
30	ACGGCGGAAA CTCACAGCTT TCGCCCAGCG AGAGGACAAA GGTCTGGAC ACACTCCAAC	660
	TGCGTCCGGA TCTTGGCTGG ATCGGACTCT CAGGGTGGAG GAGACACAAG CACAGCAGCT	720
	GCCCCAGCGTG TGCCCAGCCC TCCCACCGCT GGTCCCGGCT GCCAGGAGGC TGGCCGCTGG	780
	CGGGAAAGGGG CCGGGAAACC TCAGAGCCCC GCGGAGACAG CAGCCGCCTT GTTCTCAGC	840
35	CCGGTGGCTT TTTTTTCCCC TGCTCTCCCA GGGGACAGAC ACCACCGCCC CACCCCTCAC	900
	GCCCCACCTC CCTGGGGGAT CCTTCCGCC CCAGCCCTGA AAGCGTTAAT CCTGGAGCTT	960
	TCTGCACACC CCCCGACCGC TCCCGCCCAA GCTTCCTAAA AAAGAAAGGT GCAAAGTTG	1020
40	GTCCAGGATA GAAAATGAC TGATCAAAGG CAGGCATAAC TTCTGTGTC CGGGACGCTA	1080
	TATATAACGT GATGAGCGCA CGGGCTGCGG AGACCGACCG GAGCGCTCGC CCAGCCGCCG	1140
	CCTCCAAGCC CCTGAGGTTT CGGGGGACCA CA ATG AAC AAG TTG CTG TGC TGC	1193

Met Asn Lys Leu Leu Cys Cys

45 -20 -15

50	GCG CTC GTG GTAAAGTCCCT GGGCCAGCCG ACGGGTGCCG GGCGCCTGGG	1242
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Ala Leu Val

55	GAGGCTGCTG CCACCTGGTC TCCCAACCTC CCAGCGGACC GGCGGGAAA AAGGCTCCAC	1302
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TCGCTCCCTC CCAAG

1317

5 (2) INFORMATION FOR SEQUENCE ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH :

(B) TYPE : nucleic acid

(C) STRANDEDNESS : double

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : human OCIF genomic DNA-2

15 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 105:

GCTTACTTTG TGCCAAATCT CATTAGGCTT AAGGTAATAC AGGACTTTGA GTCAAATGAT	060
ACTGTTGCAC ATAAGAACAA ACCTATTTC ATGCTAAGAT GATGCCACTG TGTTCCCTTC	120
TCCTTCTAG TTT CTG GAC ATC TCC ATT AAG TGG ACC ACC CAG GAA ACG TTT	171

Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr Phe			
-10	-5		-1 1
	-1 1		

CCT CCA AAG TAC CTT CAT TAT GAC GAA GAA ACC TCT CAT CAG CTG TTG	219
Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu Leu	
5 10 15	

TGT GAC AAA TGT CCT CCT GGT ACC TAC CTA AAA CAA CAC TGT ACA GCA	267
Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala	
20 25 30 35	

AAG TGG AAG ACC GTG TGC GCC CCT TGC CCT GAC CAC TAC TAC ACA GAC	315
Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp	
40 45 50	

AGC TGG CAC ACC AGT GAC GAG TGT CTA TAC TGC AGC CCC GTG TGC AAG	363
Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys	
55 60 65	

GAG CTG CAG TAC GTC AAG CAG GAG TGC AAT CGC ACC CAC AAC CGC GTG	411
Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val	
70 75 80	

	TGC GAA TGC AAG GAA GGG CGC TAC CTT GAG ATA GAG TTC TGC TTG AAA	459
	Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys	
5	85	90
		95
	CAT AGG AGC TGC CCT CCT GGA TTT GGA GTG GTG CAA GCT G GTACGTGTCA	509
10	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala	
	100	105
		110
	ATGTGCAGCA AAATTAAATTA GGATCATGCA AACTCAGATA GTTGTGACAG TTTAGGAGAA	569
15	CACTTTGTT CTGATGACAT TATAGGATAG CAAATTGCAA AGGTAATGAA ACCTGCCAGG	629
	TAGGTACTAT GTGTCTGGAG TGCTTCCAAA GGACCATTGC TCAGAGGAAT ACTTGCCAC	689
	TACAGGGCAA TTTAATGACA AATCTCAAAT GCAGCAAATT ATTCTCTCAT GAGATGCATG	749
20	ATGGTTTTT TTTTTTTTT TAAAGAAAACA AACTCAAGTT GCACTATTGA TAGTTGATCT	809
	ATACCTCTAT ATTCACHTC AGCATGGACA CCTTCAAACG GCAGCACTT TTGACAAACAA	869
	TCAGAAATGT TAATTTATAC CAAGAGAGTA ATTATGCTCA TATTAATGAG ACTCTGGAGT	929
	GCTAACAAATA AGCAGTTATA ATTAATTATG TAAAAAAATGA GAATGGTGAG GGGAAATTGCA	989
25	TTTCATTATT AAAAACAAAGG CTAGTTCTTC CTTAGCATG GGAGCTGAGT GTTTGGGAGG	1049
	GTAAGGACTA TAGCAGAACAT TCTTCAATGA GCTTATTCTT TATCTTAGAC AAAACAGATT	1109
	GTCAAGCCAA GAGCAAGCAC TTGCCTATAA ACCAAGTGCT TTCTTTTG CATTGAAAC	1169
30	AGCATTGGTC AGGGCTCATG TGTATTGAAT CTTTAAACC AGTAACCCAC GTTTTTTTC	1229
	TGCCACATTT GCGAAGCTTC AGTGCAGCCT ATAACCTTTC ATAGCTTGAG AAAATTAAAGA	1289
	GTATCCACTT ACTTAGATGG AAGAAGTAAT CAGTATAGAT TCTGATGACT CAGTTGAA	1349
	CAGTGTTC CAACTGAAGC CCTGCTGATA TTTAAGAAA TATCTGGATT CCTAGGCTGG	1409
35	ACTCCTTTT GTGGGAGCT GTCCTGCGCA TTGAGAATT TTGGCAGCAC CCCTGGACTC	1469
	TAGCCACTAG ATACCAATAG CAGTCCTTCC CCCATGTGAC AGCCAAAAT GTCTCAGAC	1529
	ACTGTCAAAT GTGCCAGGT GGAAATCA CTCTGGTTG AGAACAGGGT CATCAATGCT	1589
40	AAGTATCTGT AACTATTTA ACTCTAAAAA CTTGTGATAT ACAAAAGTCTA AATTATTAGA	1649
	CGACCAATAC TTAGGTTTA AAGGCATACA AATGAAACAT TCAAAATCA AAATCTATT	1709
	TGTTCTCAA ATAGTGAATC TTATAAAATT AATCACAGAA GATGCAAATT GCATCAGAGT	1769
	CCCTAAAT TCCTCTTCGT ATGAGTATTG GAGGGAGGAA TTGGTGATAG TTCTACTTT	1829
45	CTATTGGATG GTACTTTGAG ACTCAAAAGC TAAGCTAAGT TGTGTGTG TGAGGGTGC	1889
	GGGTGTGGAA TCCCCTCAGA TAAAAGCAA TCCATGTAAT TCATTGAGTA AGTTGTATAT	1949
	GTAGAAAAAT GAAAAGTGGG CTATGCAGCT TGAAACTAG AGAATTGAAA AAAATAATGG	2009
50	AAATCACAAG GATCTTTCTT AAATAAGTAA GAAAATCTGT TTGTAGAATG AAGCAAGCAG	2069
	GCAGCCAGAA GACTCAGAAC AAAAGTACAC ATTTACTCT GTGTACACTG GCAGCACAGT	2129
	GGGATTATT TACCTCTCCC TCCCTAAAAA CCCACACAGC GGTTCCCTTT GGGAAATAAG	2189

	AGGTTTCCAG CCCAAAGAGA AGGAAAGACT ATGTGGTGT ACTCTAAAAA GTATTTAATA	2249
5	ACCGTTTGT TGTTGCTGTT GCTGTTTGA AATCAGATTG TCTCCTCTCC ATATTTATT	2309
	TACTTCATTC TCTTAATTCC TGTGGAATT CTTAGAGCAA GCATGGTGA TTCTCAACTG	2369
	TAAAGCCAAA TTTCTCCATC ATTATAATT CACATTTCGC CTGGCAGGTT ATAATTTTA	2429
10	TATTTCCACT GATAGTAATA AGGTAAAATC ATTACTTAGA TGGATAGATC TTTTCATAAA	2489
	AAAGTACCAT CAGTTATAGA GGGAAAGTCAT GTTCATGTT AGGAAGGTCA TTAGATAAAG	2549
	CTTCTGAATA TATTATGAAA CATTAGTTCT GTCATTCTTA GATTCTTTT GTTAAATAAC	2609
	TTTAAAAGCT AACTTACCTA AAAGAAATAT CTGACACATA TGAACCTCTC ATTAGGATGC	2669
15	AGGAGAAGAC CCAAGCCACA GATATGTATC TGAAGAATGA ACAAGATTCT TAGGCCCGGC	2729
	ACGGTGGCTC ACATCTGAA TCTCAAGAGT TTGAGAGGTC AAGGCGGGCA GATCACCTGA	2789
	GGTCAGGAGT TCAAGACCAG CCTGGCCAAC ATGATGAAAC CCTGCCTCTA CTAAAATAC	2849
	AAAAATTAGC AGGGCATGGT GGTGCATGCC TGCAACCTA GCTACTCAGG AGGCTGAGAC	2909
20	AGGAGAATCT CTTGAACCCCT CGAGGCGGAG GTTGTGGTGA GCTGAGATCC CTCTACTGCA	2969
	CTCCAGCCTG GGTGACAGAG ATGAGACTCC GTCCCTGCCG CCGCCCCCGC CTCCCCCCC	3029
	AAAAAGATTG TTCTTCATGC AGAACATACG GCAGTCACA AAGGGAGACC TGGGTCCAGG	3089
	TGTCCAAGTC ACTTATTTCG AGTAAATTAG CAATGAAAGA ATGCCATGGA ATCCCTGCC	3149
25	AAATACCTCT GCTTATGATA TTGAGAATT TGATATAGAG TTGTATCCCA TTTAAGGAGT	3209
	AGGATGTAGT AGGAAAGTAC TAAAAACAAA CACACAAACA GAAAACCTC TTTGTTTGT	3269
	AAGGTGGTTC CTAAGATAAT GTCAGTGCAA TGCTGAAAT AATATTAAT ATGTGAAGGT	3329
	TTTAGGCTGT GTTTCCCT CCTGTTCTT TTTCTGCCA GCCCTTGTC ATTTTGAG	3389
30	GTCAATGAAT CATGTAGAAA GAGACAGGAG ATGAAACTAG AACCACTCA TTTGCC	3449
	TTTTTATTT TCTGGTTTG GTAAAGATA CAATGAGGTA GGAGGTTGAG ATTTATAAAT	3509
	GAAGTTTAAT AAGTTCTGT AGCTTGATT TTTCTTTTC ATATTTGTTA TCTGCATAA	3569
35	GCCAGAATTG GCCTGTAAAA TCTACATATG GATATTGAAG TCTAAATCTG TTCAACTAGC	3629
	TTACACTAGA TGGAGATATT TTCATATTCA GATACACTGG AATGTATGAT CTAGCCATGC	3689
	GTAATATAGT CAAGTGTGTTG AAGGTATTAA TTTTTAATAG CGTCTTAGT TGTGGACTGG	3749
40	TTCAAGTTT TCTGCCAATG ATTTCTTCAA ATTTATCAA TATTTTCCA TCATGAAGTA	3809
	AAATGCCCTT GCAGTCACCC TTCCGTAAAGT TTGAACGACT CTGCTGTTT AAACAGTTA	3869
	AGCAAATGGT ATATCATCTT CCGTTTACTA TGAGCTTAA CTGCAGGCTT ACGCTTTGA	3929
	GTCAGCGGCC AACTTTATTG CCACCTTCAA AAGTTTATTA TAATGTTGTA AATTTTACT	3989
45	TCTCAAGGTT AGCATACTTA GGAGTTGCTT CACAATTAGG ATTCAAGGAA GAAAGAACTT	4049
	CAGTAGGAAC TGATTGGAAT TTAATGATGC AGCATTCAAT GGGTACTAAT TTCAAAGAAAT	4109
	GATATTACAG CAGACACACA GCAGTTATCT TGATTTCTA GGAATAATTG TATGAAGAAT	4169
	ATGGCTGACA ACACGGCCTT ACTGCCACTC AGCGGAGGCT GGACTAATGA ACACCCCTACC	4229
50	CTTCTTCCT TTCCCTCTCAC ATTTCATGAG CGTTTGTAG GTAACGGAGAA AATTGACTTG	4289
	CATTGCAATT ACAAGGAGGA GAAACTGGCA AAGGGGATGA TGGTGAAGT TTTGTTCTGT	4349

	CTAATGAAGT GAAAAATGAA AATGCTAGAG TTTGTGCAA CATAATAGTA GCAGTAAAAA	4409
	CCAAGTGAAA AGTCTTCCA AACTGTGTT AAGAGGGCAT CTGCTGGAA ACGATTGAG	4469
5	GAGAAGGTAC TAAATTGCTT GGTATTTCC GTAG GA ACC CCA GAG CGA AAT ACA	4523
	Gly Thr Pro Glu Arg Asn Thr	
	115	
10	GTT TGC AAA AGA TGT CCA GAT GGG TTC TTC TCA AAT GAG ACG TCA TCT	4571
	Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser	
	120 125 130 135	
15	AAA GCA CCC TGT AGA AAA CAC ACA AAT TGC AGT GTC TTT GGT CTC CTG	4619
	Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu	
20	140 145 150	
	CTA ACT CAG AAA GGA AAT GCA ACA CAC GAC AAC ATA TGT TCC GGA AAC	4667
	Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn	
25	155 160 165	
	AGT GAA TCA ACT CAA AAA TGT GGA ATA G GTAATTACAT TCCAAAATAC	4715
	Ser Glu Ser Thr Gln Lys Cys Gly Ile	
30	170 175	
	GTCTTGTAC GATTTGTAG TATCATCTCT CTCTCTGAGT TGAACACAAG GCCTCCAGCC	4775
	ACATTCTGG TCAAACCTAC ATTTCCCTT TCTGAATCT TAACCAGCTA AGGCTACTCT	4835
35	CGATGCCATTA CTGCTAAAGC TACCACTCAG AATCTCTCAA AAACCTCATCT TCTCACAGAT	4895
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40	AAGGGCAGTG TCAAGTTGC CACTGAGATG AAATTAGGAG AGTCCAAACT GTAGAATTCA	5015
	CGTTGTGTGT TATTACTTTC ACGAATGTCT GTATTATTAA CTAAAGTATA TATTGGCAAC	5075
	TAAGAAGCAA AGTGATATAA ACATGATGAC AAATTAGGCC AGGCATGGTG GCTTACTCCT	5135
	ATAATCCCAA CATTGGGG GGCAAGGTA GGCAAGATCAC TTGAGGTCA GATTCAAGA	5195
45	CCAGCCTGAC CAACATGGTG AACCTTGTC TCTACTAAAA ATACAAAAT TAGCTGGCA	5255
	TGGTAGCAGG CACTTCTAGT ACCAGCTACT CAGGGCTGAG GCAGGAGAAT CGCTTGAACC	5315
	CAGGAGATGG AGGTTGCAGT GAGCTGAGAT TGTACCACTG CACTCCAGTC TGGGCAACAG	5375
50	AGCAAGATTT CATCACACAC ACACACACAC ACACACACAC ACACATTAGA AATGTGTACT	5435
	TGGCTTGTGTT ACCTATGGTA TTAGTGCATC TATTGCATGG AACTTCCAAG CTACTCTGGT	5495
	TGTGTTAACG TCTTCATTGG GTACAGGTCA CTAGTATTAA GTTCAGGTTA TTCGGATGCA	5555

	TTCCACGGTA GTGATGACAA TTCATCAGGC TAGTGTGTGT GTTCACCTTG TCACTCCCCAC	5615		
5	CACTAGACTA ATCTCAGACC TTCACTCAAA GACACATTAC ACTAAAGATG ATTTGCTTT	5675		
	TTGTGTTAA TCAAGCAATG GTATAAACCA GCTTGACTCT CCCCAAACAG TTTTCGTAC	5735		
	TACAAAGAAG TTATGAAGC AGAGAAATGT GAATTGATAT ATATATGAGA TTCTAACCCA	5795		
10	GTTCCAGCAT TGTTTCATTG TGTAATTGAA ATCATAGACA AGCCATTAA GCCTTGCTT	5855		
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	TTTAACATTC TCTTAATTA ATTCATTTT AATTTACTT TTTTCATT ATTGTGCACT	5975		
	TACTATGTGG TACTGTGCTA TAGAGGTTT AACATTATA AAAACACTGT GAAAGTTGCT	6035		
15	TCAGATGAAT ATAGGTAGTA GAACGGCAGA ACTAGTATTCA AAAGCCAGGT CTGATGAATC	6095		
	CAAAAACAAA CACCCATTAC TCCCATTTC TGGAACATAC TTACTCTACC CAGATGCTCT	6155		
	GGGCTTGTA ATGCCATGT AAATAACATA GTTTATGTT TGGTTATTT CCTATGTAAT	6215		
	GTCTACTTAT ATATCTGTAT CTATCTCTT CTTTGTTC CAAAGGTAAC TATGTGTCTA	6275		
20	AATGTGGCA AAAAATAACA CACTATTCCA AATTACTGTT CAAATTCTT TAAGTCAGTG	6335		
	ATAATTATTT GTTTGACAT TAATCATGAA GTTCCCTGTG GGTACTAGGT AAACCTTAA	6395		
	TAGAATGTTA ATGTTGTAT TCATTATAAG AATTTTGGC TGTTACTTAT TTACAACAAT	6455		
	ATTTCACTCT AATTAGACAT TTACTAAACT TTCTCTGAA AACATGCC AAAAAGAAC	6515		
25	ATTAGAAGAC ACCTAAGCTC AGTTGGTCTC TGCCACTAAG ACCAGCCAAC AGAAGCTTGA	6575		
	TTTTATTCAA ACTTTGCATT TTAGCATATT TTATCTGGA AAATTCAATT GTGTGGTTT	6635		
	TTTGTGTTTG TTTGTATTGA ATAGACTCTC AGAAATCCAA TTGTTGAGTA AATCTTCTGG	6695		
30	GTGTTCTAAC CTTCTTTAG AT GTT ACC CTG TGT GAG GAG GCA TTC TTC AGG	6747		
	Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg			
	180	185		
35	TTT GCT GTT CCT ACA AAG TTT ACG CCT AAC TGG CTT AGT GTC TTG GTA	6795		
	Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val			
	190	195	200	
40	GAC AAT TTG CCT GGC ACC AAA GTA AAC GCA GAG AGT GTA GAG AGG ATA	6843		
	Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile			
	205	210	215	
45	AAA CGG CAA CAC AGC TCA CAA GAA CAG ACT TTC CAG CTG CTG AAG TTA	6891		
	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu			
	220	225	230	235
50	TGG AAA CAT CAA AAC AAA GAC CAA GAT ATA GTC AAG AAG ATC ATC CAA G	6940		

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln

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	GTAATTACAT TCCAAAATAC GTCTTGTAC GATTTGTAG TATCATCTCT CTCTCTGAGT	7000
	TGAACACAAG GCCTCCAGCC ACATTCTGG TCAAACATTAC ATTTTCCCTT TCTTGAATCT	7060
10	TAACCAGCTA AGGCTACTCT CGATGCATTA CTGCTAAAGC TACCACTCAG AATCTCTCAA	7120
	AAACTCATCT TCTCACAGAT AACACCTCAA AGCTTGATTTC TCTCTCCTTT CACACTGAAA	7180
	TCAAATCTTG CCCATAGGCA AAGGGCAGTG TCAAGTTTGC CACTGAGATG AAATTAGGAG	7240
15	AGTCCAAACT GTAGAATTCA CGTTGTGTGT TATTACTTTC ACCAATGTCT GTATTATTAA	7300
	CTAAAGTATA TATTGGCAAC TAAGAACAA AGTGTATATA ACATGATGAC AAATTAGGCC	7360
	AGGCATGGTG GCTTACTCCT ATAATCCAA CATTGGGG GGCAAGGTA GGCAGATCAC	7420
	TTGAGGTCAG GATTTCAGA CCAGCTGAC CAACATGGTG AAACCTTGTCT TCTACTAAAA	7480
20	ATACAAAAAT TAGCTGGGCA TGGTAGCAGG CACTTCTAGT ACCAGCTACT CAGGGCTGAG	7540
	GCAGGAGAAAT CGCTTGAACC CAGGAGATGG AGGTTGCAGT GAGCTGAGAT TGTACCACTG	7600
	CACTCCAGTC TGGGCAACAG AGCAAGATTT CATCACACAC ACACACACAC ACACACACAC	7660
	ACACATTAGA AATGTGTACT TGGTTTGTGTT ACCTATGGTA TTAGTGCATC TATTGCATGG	7720
25	AACTCCAAG CTACTCTGGT TGTGTTAACG TCTTCATTGG GTACAGGTCA CTAGTATTAA	7780
	GTTCAAGGTTA TTGGATGCA TTCCACGGTA GTGATGACAA TTCATCAGGC TAGTGTGTGT	7840
	GTTCACCTTG TCACTCCCAC CACTAGACTA ATCTCAGACC TTCACTCAA GACACATTAC	7900
30	ACTAAAGATG ATTTCGTTTT TTGTTGTTAA TCAAGCAATG GTATAAACCA GCTTGAETCT	7960
	CCCCAAACAG TTTTCGTAC TACAAAGAAG TTTATGAAGC AGAGAAATGT GAATTGATAT	8020
	ATATATGAGA TTCTAACCCA GTTCCAGCAT TGTTTCATTG TGTAAATTGAA ATCATAGACA	8080
	AGCCATTTA GCCTTGCTT TCTTATCTAA AAAAAAAA AAAAAAATGA AGGAAGGGT	8140
35	ATTAAGGAA GTGATCAAAT TTAAACATTC TCTTTAATTAA ATTCAATTTT AATTTTACTT	8200
	TTTTTCATT ATTGTGCACT TACTATGTGG TACTGTGCTA TAGAGGTTT AACATTATA	8260
	AAAACACTGT GAAAGTTGCT TCAGATGAAT ATAGGTAGTA GAACGGCAGA ACTAGTATT	8320
40	AAAGCCAGGT CTGATGAATC CAAAAACAAA CACCCATTAC TCCCATTTC TGGGACATAC	8380
	TTACTCTACC CAGATGCTCT GGGCTTGTA ATGCCTATGT AAATAACATA GTTTTATGTT	8440
	TGGTTATTTC CCTATGTAAT GTCTACTTAT ATATCTGTAT CTATCTCTG CTTGTTCC	8500
	AAAGGTAAAC TATGTGTCTA AATGTGGGCA AAAAATAACA CACTATTCCA AATTACTGTT	8560
45	CAAATTCCCT TAAGTCAGTG ATAATTATTGTTTGACAT TAATCATGAA GTTCCCTGTG	8620
	GGTACTAGGT AAACCTTAA TAGAATGTTA ATGTTTGTAT TCATTATAAG AATTTTGCG	8680
	TGTTACTTAT TTACAACAAT ATTTCACTCT AATTAGACAT TTACTAAACT TTCTCTGAA	8740
50	AACAATGCCA AAAAAAGAAC ATTAGAACAC ACGTAAGCTC AGTTGGTCTC TGCCACTAAG	8800
	ACCAGCCAAC AGAAGCTTGA TTTTATTCAA ACTTTGCATT TTAGCATATT TTATCTTGG	8860
	AAATTCAATT GTGTTGGTTT TTTGTTTTG TTGTATTGA ATAGACTCTC AGAAATCCAA	8920

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	TTGTTGAGTA AATCTTCTGG GTTTCTAAC CTTTCTTAG AT ATT GAC CTC TGT	Asp Ile Asp Leu Cys	8974
5			255
	GAA AAC AGC GTG CAG CGG CAC ATT GGA CAT GCT AAC CTC ACC TTC GAG		9022
10	Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu		
	260	265	270
15	CAG CTT CGT AGC TTG ATG GAA AGC TTA CCG GGA AAG AAA GTG GGA GCA		9070
	Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala		
	275	280	285
20	GAA GAC ATT GAA AAA ACA ATA AAG GCA TGC AAA CCC AGT GAC CAG ATC		9118
	Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile		
	290	295	300
25	CTG AAG CTG CTC AGT TTG TGG CGA ATA AAA AAT GGC GAC CAA GAC ACC		9166
	Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr		
	305	310	315
30	TTG AAG GGC CTA ATG CAC GCA CTA AAG CAC TCA AAG ACG TAC CAC TTT		9214
	Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe		
35	325	330	335
	CCC AAA ACT GTC ACT CAG AGT CTA AAG AAG ACC ATC AGG TTC CTT CAC		9262
	Pro Lys Thr Val Thr Gln Ser Leu Lys Thr Ile Arg Phe Leu His		
40	340	345	350
	AGC TTC ACA ATG TAC AAA TTG TAT CAG AAG TTA TTT TTA GAA ATG ATA		9310
45	Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile		
	355	360	365
50	GGT AAC CAG GTC CAA TCA GTA AAA ATA AGC TGC TTA TAACTGGAAA		9356
	Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu		
	370	375	380

	TGGCCATTGA GCTGTTTCCT CACAATTGGC GAGATCCCAT GGATGAGTAA ACTGTTTCTC	9416
5	AGGCACCTGA GGCTTCAGT GATATCTTC TCATTACCAAG TGACTAATTT TGCCACAGGG	9476
	TACTAAAAGA AACTATGATG TGGAGAAAGG ACTAACATCT CCTCCAATAA ACCCCAAATG	9536
	GTTCATCCAA CTGTCAGATC TGGATCGTTA TCTACTGACT ATATTTTCCC TTATTACTGC	9596
10	TTGCAGTAAT TCAACTGGAA ATTAAAAAAA AAAAAGTAGA CTCCACTGGG CCTTACTAAA	9656
	TATGGGAATG TCTAACCTAA ATAGCTTGG GATTCCAGCT ATGCTAGAGG CTTTATTAG	9716
	AAAGCCATAT TTTTTCTGT AAAAGTTACT AATATATCTG TAACACTATT ACAGTATTGC	9776
15	TATTTATATT CATTAGATA TAAGATTGG ACATATTATC ATCCTATAAA GAAACGGTAT	9836
	GACTTAATT TAGAAAGAAA ATTATATTCT GTTTATTATG ACAAAATGAAA GAGAAAATAT	9896
	ATATTTTAA TGGAAAGTTT GTAGCATTTT TCTAATAGGT ACTGCCATAT TTTCTGTGT	9956
	GGAGTATTTT TATAATTAA TCTGTATAAG CTGTAATATC ATTTTATAGA AAATGCATTA	10016
20	TTTAGTCAAT TGTTAATGT TGGAAAACAT ATGAAATATA AATTATCTGA ATATTAGATG	10076
	CTCTGAGAAA TTGAATGTAC CTTATTAAA AGATTTATG GTTTATAAC TATATAATG	10136
	ACATTATTAA AGTTTCAA TTATTTTTA TTGCTTCTC TGTTGCTTT ATTT	10190

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Claims

30 1. A protein characterized by the following properties:

(a) molecular weights on SDS-polyacrylamide gel electrophoresis (SDS-PAGE)

; approximately 60 kD under reducing conditions

35 ; approximately 60 kD and 120 kD under non-reducing conditions

(b) a high affinity to cation-exchange column and heparin column

(c) a biological activity to inhibit osteoclast differentiation and/or maturation

40 ; its activity is decreased by heating at 70°C for 10 min or at 56°C for 30 min.

; its activity is lost by heating at 90 °C for 10 min

(d) internal amino acid sequences provided in sequence numbers 1, 2, and 3.

45 2. A protein of claim 1 having N-terminal amino acid sequences provided in sequence number 7.

3. A protein of claim 1 produced in human fibroblasts.

50 4. A method of producing the protein of claim 1, 2, and 3 by the following process: cultivating human fibroblasts ; purifying the protein by a combination of ion-exchange column, affinity-column and reverse phase-column chromatography.

55 5. A method of producing the protein of claim 4 by cultivating human fibroblasts on alumina ceramic pieces.

6. A protein with amino acid sequence provided in sequence number 4.

7. cDNAs encoding amino acid sequence provided in sequence number 4.

8. cDNA with nucleotide sequence provided in sequence number 6.
9. cDNAs that hybridize to cDNA provided in sequence number 6 under moderately stringent conditions.
- 5 10. A protein expressed from cDNA encoding amino acid sequence provided in sequence number 4.
11. A protein with a biological activity to inhibit osteoclast differentiation and/or maturation, that obtain as amino acid expressed cDNA sharing at least 80 % sequence identity with the amino acid sequence provided in sequence number 4.
- 10 12. A method of production of the protein with the following properties and inhibit osteoclast differentiation and/or maturation by gene engineering using cDNA encoding amino acid sequence provided in sequence number 4:
 - (a) molecular weights on SDS-polyacrylamide gel electrophoresis (SDS-PAGE)
 - 15 ; approximately 60 kD under reducing conditions
 - ; approximately 60 kD and 120 kD under non-reducing conditions
 - (b) a high affinity to cation-exchange column and heparin column
 - 20 (c) ; inhibit osteoclast differentiation and/or maturation activity is decreased by heating at 70°C for 10 min or at 56°C for 30 min
 - ; its activity is lost by heating at 90 °C for 10 min
 - (d) internal amino acid sequence provided in sequence number 1-3.
13. A method of producing the protein according to claim 10 by gene engineering using mammalian cells as host cells.
14. A method of producing the protein according to claim 13 by gene engineering using 293/EBNA cells or CHO cells as mammalian host cells.
15. A cDNA with nucleotide sequence provided in sequence number 8.
16. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 8.
- 35 17. cDNAs encoding amino acid sequence provided in sequence number 9.
18. A cDNA with nucleotide sequence provided in sequence number 10.
- 40 19. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 10.
20. cDNAs encoding amino acid sequence provided in sequence number 11.
21. A cDNA with nucleotide sequence provided in sequence number 12.
- 45 22. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 12.
23. cDNAs encoding amino acid sequence provided in sequence number 13.
- 50 24. A cDNA with nucleotide sequence provided in sequence number 14.
25. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 14.
26. cDNAs encoding amino acid sequence provided in sequence number 15.
- 55 27. A cDNA with nucleotide sequence provided in sequence number 83.
28. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 83.

29. cDNAs encoding amino acid sequence provided in sequence number 62.
30. A cDNA with nucleotide sequence provided in sequence number 84.
- 5 31. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 84.
32. cDNAs encoding amino acid sequence provided in sequence number 63.
33. A cDNA with nucleotide sequence provided in sequence number 85.
- 10 34. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 85.
35. cDNAs encoding amino acid sequence provided in sequence number 64.
- 15 36. A cDNA with nucleotide sequence provided in sequence number 86.
37. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 86.
38. cDNAs encoding amino acid sequence provided in sequence number 65.
- 20 39. A cDNA with nucleotide sequence provided in sequence number 87.
40. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 87.
- 25 41. cDNAs encoding amino acid sequence provided in sequence number 66.
42. A cDNA with nucleotide sequence provided in sequence number 88.
43. A protein encoded by a cDNA having a sequence provided in sequence number 88.
- 30 44. cDNAs encoding amino acid sequence provided in sequence number 67.
45. A cDNA with nucleotide sequence provided in sequence number 89.
- 35 46. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 89.
47. cDNAs encoding amino acid sequence provided in sequence number 68.
48. A cDNA with nucleotide sequence provided in sequence number 90.
- 40 49. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 90.
- 50 50. cDNAs encoding amino acid sequence provided in sequence number 69.
- 45 51. A cDNA with nucleotide sequence provided in sequence number 91.
52. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 91.
53. cDNAs encoding amino acid sequence provided in sequence number 70.
- 50 54. A cDNA with nucleotide sequence provided in sequence number 92.
55. A protein encoded by a cDNA having a nucleotide sequence provided in number 92.
- 55 56. cDNAs encoding amino acid sequence provided in sequence number 71.
57. A cDNA with nucleotide sequence provided in sequence number 93.

58. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 93.
59. cDNAs encoding amino acid sequence provided in sequence number 72.
- 5 60. A cDNA with nucleotide sequence provided in sequence number 94.
61. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 94.
62. cDNAs encoding amino acid sequence provided in sequence number 73.
- 10 63. A cDNA with nucleotide sequence provided in sequence number 95.
64. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 95.
- 15 65. cDNAs encoding amino acid sequence provided in sequence number 74.
66. A cDNA with nucleotide sequence provided in sequence number 96.
67. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 96.
- 20 68. cDNAs encoding amino acid sequence provided in sequence number 75.
69. A cDNA with nucleotide sequence provided in sequence number 97.
- 25 70. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 97.
71. cDNAs encoding amino acid sequence provided in sequence number 76.
72. A cDNA with nucleotide sequence provided in sequence number 98.
- 30 73. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 98.
74. cDNAs encoding amino acid sequence provided in sequence number 77.
- 35 75. A cDNA with nucleotide sequence provided in sequence number 99.
76. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 99.
77. cDNAs encoding amino acid sequence provided in sequence number 78.
- 40 78. A cDNA with nucleotide sequence provided in sequence number 100.
79. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 100.
- 45 80. cDNAs encoding amino acid sequence provided in sequence number 79.
81. A cDNA with nucleotide sequence provided in sequence number 101.
82. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 101.
- 50 83. cDNAs encoding amino acid sequence provided in sequence number 80.
84. A cDNA with nucleotide sequence provided in sequence number 102.
- 55 85. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 102.
86. cDNAs encoding amino acid sequence provided in sequence number 81.

87. A cDNA with nucleotide sequence provided in sequence number 103.
88. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 103.
- 5 89. cDNAs encoding amino acid sequence provided in sequence number 82.
90. Genomic DNAs encoding the amino acid sequence provided in sequence number 4.
91. Genomic DNAs of Claim 90 with the nucleotide sequence provided in sequence number 104 or 105.
- 10 92. An antibody having specific affinity to the OCIF
93. An antibody of Claim 92 that is polyclonal antibody.
- 15 94. An antibody of Claim 92 that is monoclonal antibody.
95. A monoclonal antibody of Claim 94 being characterized by the following properties.
Molecular weight of about 150,000, and of subclass IgG₁, IgG_{2a}, or IgG_{2b}.
- 20 96. A method of determining the concentration of the protein of the OCIF using the antibodies of Claim 92, 93, 94, and 95.

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Fig. 1

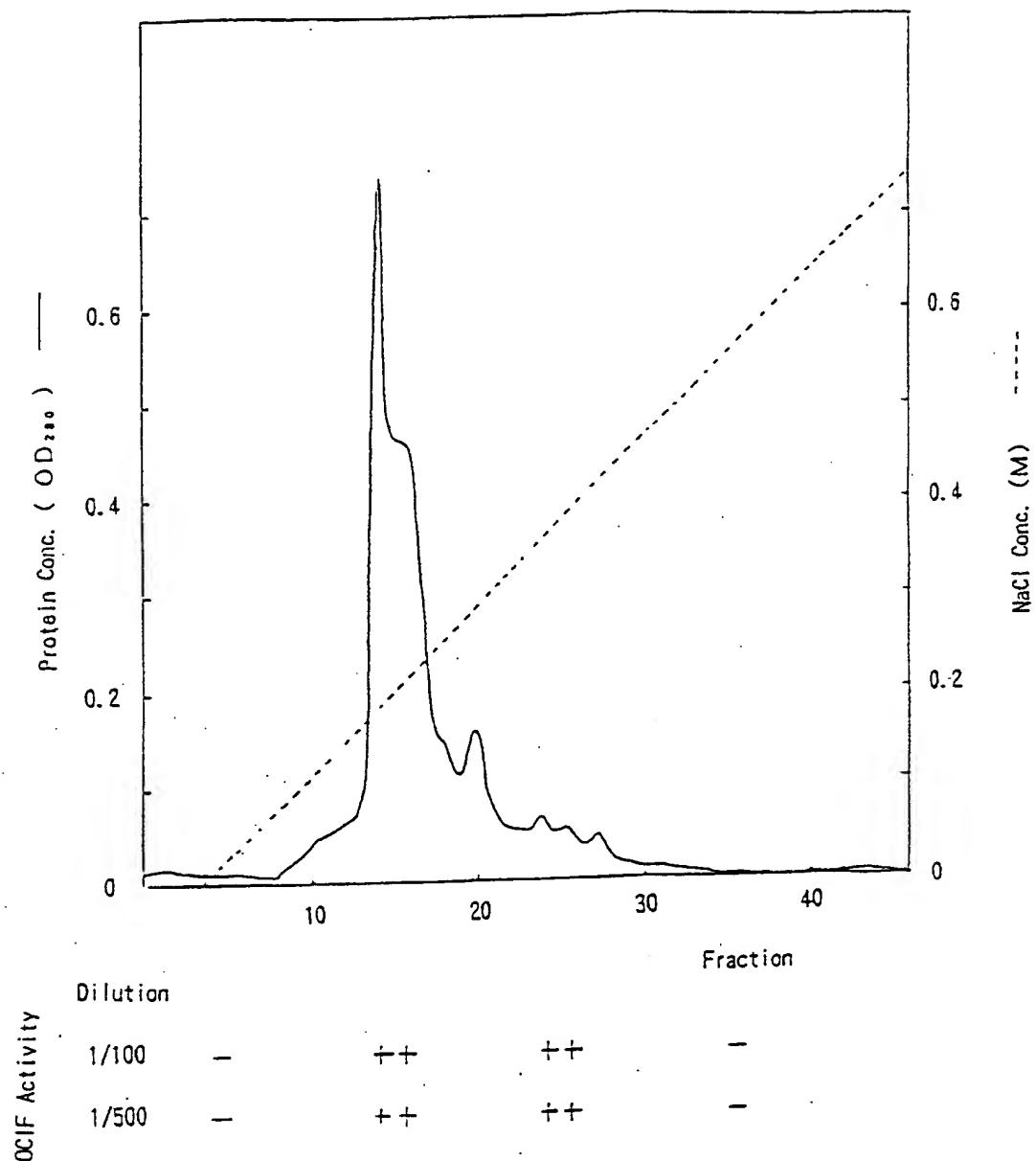


Fig. 2

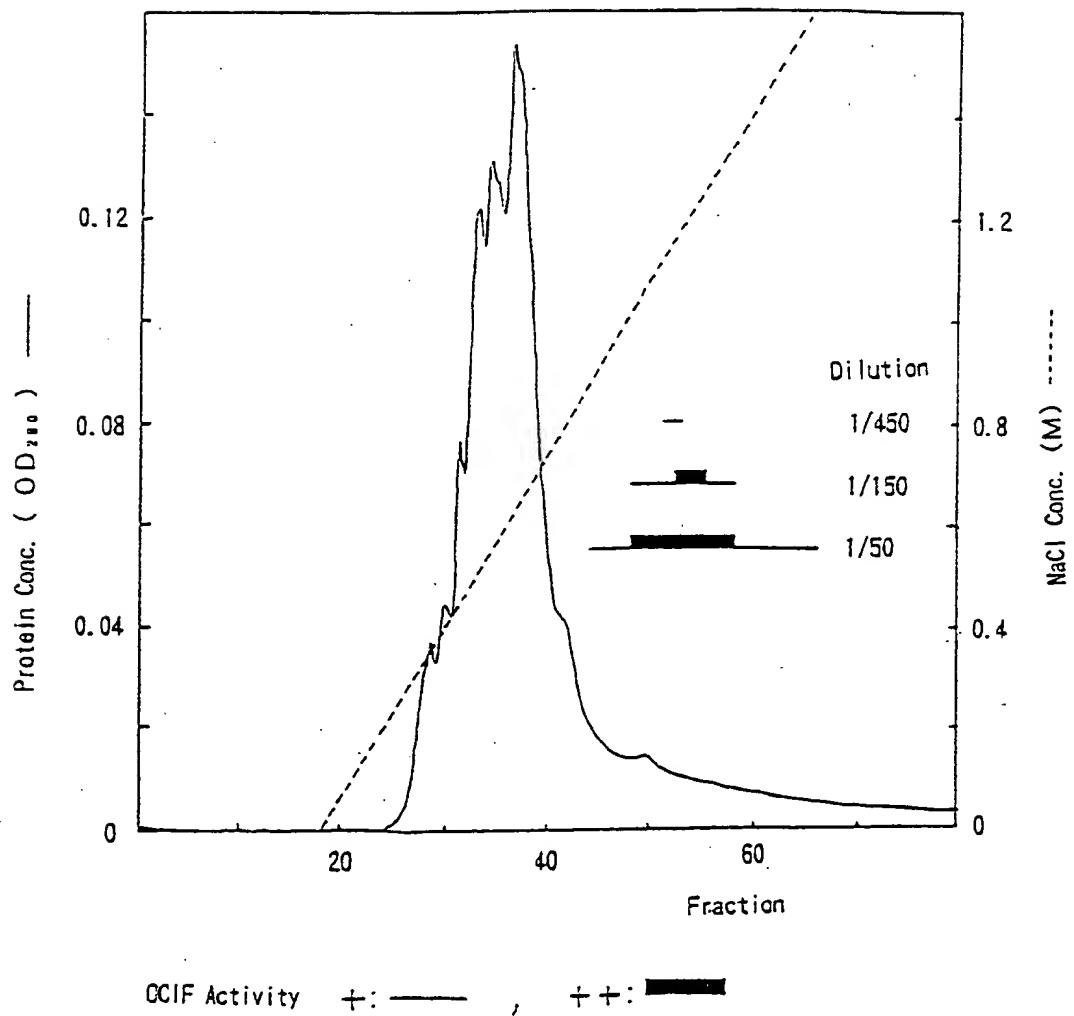


Fig. 3

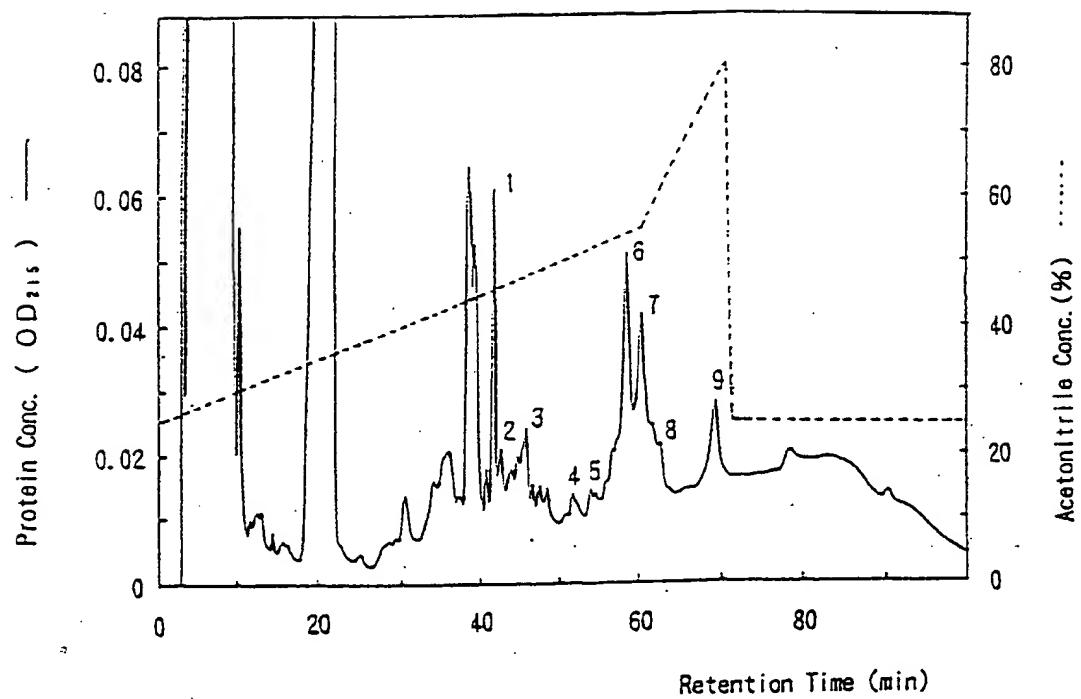


Fig. 4

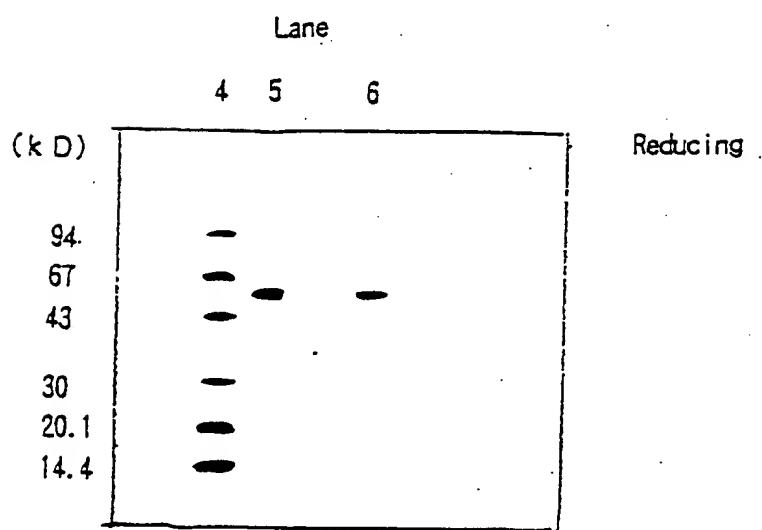
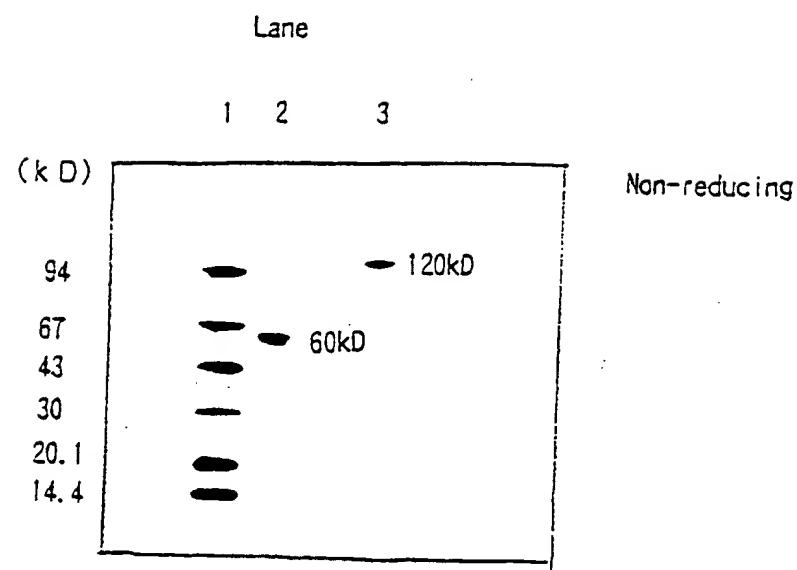


Fig.5

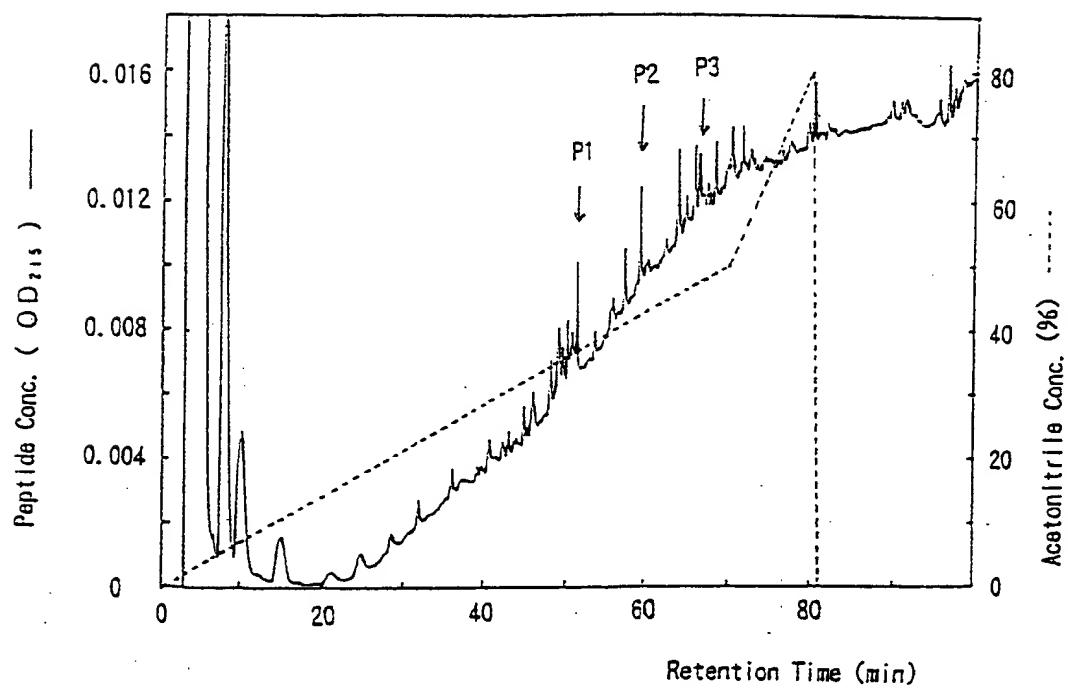


Fig. 6

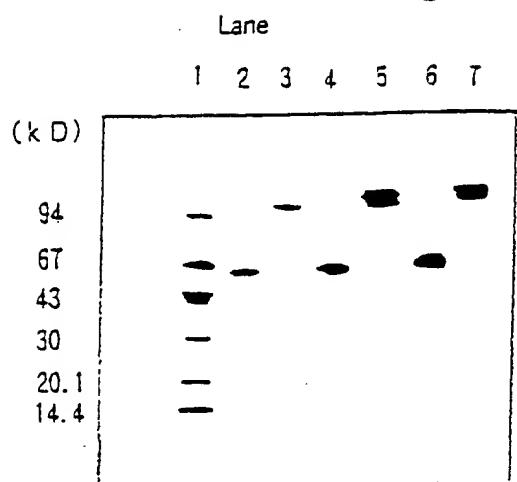


Fig. 7

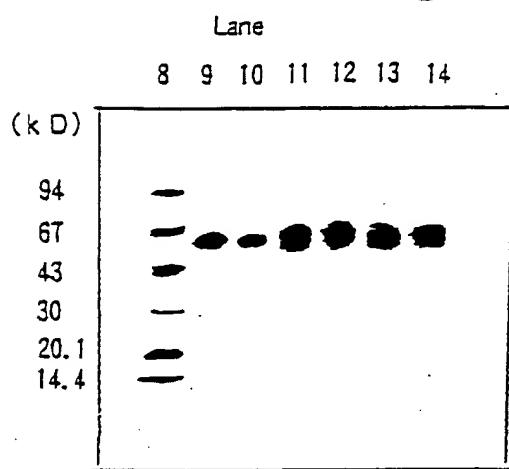


Fig. 8

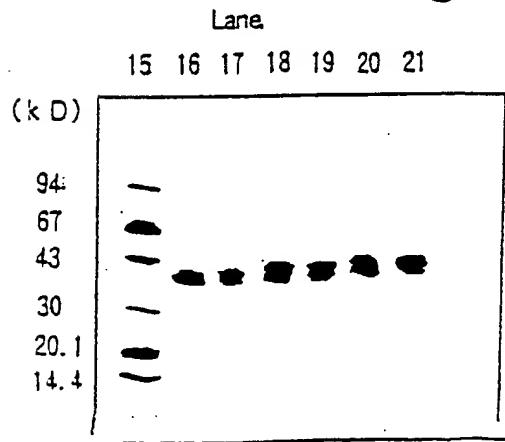


Fig. 9

1
MNNLLCCALVFLDISIKWTTQETFPPKYLHYDEETSHQLLCOKCPPGTYLKQHCTAKWKT (OCIF1)

MNNLLCCALVFLDISIKWTTQETFPPKYLHYDEETSHQLLCOKCPPGTYLKQHCTAKWKT (OCIF2)

1
61
VCAPCPDHYYTDSWHTSDECLYCSPECVELQYVKQECNRTHNRVCECKEGRYLEIEFCLK (OCIF1)

VCAPCPDHYYTDSWHTSDECLYCSPEC-----CNRTHNRVCECKEGRYLEIEFCLK (OCIF2)
61
121
HRSCPFGVVQAGTPERNTVKRCPDGFFSNETSSKAPCRKHTNCVFGLLLTKGNAT (OCIF1)

HRSCPFGVVQAGTPERNTVKRCPDGFFSNETSSKAPCRKHTNCVFGLLLTKGNAT (OCIF2)
114
181
HDNCSGNSESTQKCGIDVTLCLEEAFFRFAVPTKFTPWNLSVLVDNLPGTKVNAESVERI (OCIF1)

HDNCSGNSESTQKCGIDVTLCLEEAFFRFAVPTKFTPWNLSVLVDNLPGTKVNAESVERI (OCIF2)
174
241
KRQHSSQEQTFLQLLKLWKHQNKDQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLME (OCIF1)

KRQHSSQEQTFLQLLKLWKHQNKDQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLME (OCIF2)
234
301
SLPGKKVGAEDIEKTIKACKPSOQILKLLSLWRIKNGDQDTLKGLMHALKHSKYHFPKT (OCIF1)

SLPGKKVGAEDIEKTIKACKPSOQILKLLSLWRIKNGDQDTLKGLMHALKHSKYHFPKT (OCIF2)
294
361
VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL (OCIF1)

VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL (OCIF2)
354

Fig. 10

1
MNNLLCCALVFLDISIKWTTQETFPPKYLHYDEETSHQLLCOKCPPGTYLKQHCTAKWKT (OCIF1)

MNKLLCCALVFLDISIKWTTQETFPPKYLHYDEETSHQLLCOKCPPGTYLKQHCTAKWKT (OCIF3)
1

61
VCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLK (OCIF1)

VCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLK (OCIF3)
61

121
HRSCPPGFVVQAGTPERNTVKRCPOGFFSNETSSKAPCRKHTNCVFGLLLTKGNAT (OCIF1)

HRSCPPGFVVQAGTPERNTVKRCPOGFFSNETSSKAPCRKHTNCVFGLLLTKGNAT (OCIF3)
121

181
HDNICSGNSESTQKCGIDVTLCLEEAFFRFAVPTKFTPWNLSVLVDNLPGTKVN AESVERI (OCIF1)

HDNICSGNSESTQKCGIDVTLCLEEAFFRFAVPTKFTPWNLSVLVDNLPGTKVN AESVERI (OCIF3)
181

241
KRQHSSQEQTFLQLLKLWKHQNKDQDIVERKIIQDIDLCENS VQRHIGHANLT FEQLRSLME (OCIF1)

KRQHSSQEQTFLQLLKLWKHQNKDQDIVERKIIQDIDLCENS VQRHIGHANLS----- (OCIF3)
241

301
SLPGKKVGAEDIEKTIKACKPSDQILKLLSLWRIKNGDQDTLKGLMHALKHSKYHFPKT (OCIF1)

-----LWRIKNGDQDTLKGLMHALKHSKYHFPKT (OCIF3)
292

361
VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL (OCIF1)

VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL (OCIF3)
322

Fig. 11

1
MNNLLCCALVFLDISIKWTTQETFPPKYLHYDEETSHQLLCOKCPPGTYLKQHCTAKWKT (OCIF1)

MNKLLCCSLVFLDISIKWTTQETFPPKYLHYDEETSHQLLCOKCPPGTYLKQHCTAKWKT (OCIF4)
1
61
VCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLK (OCIF1)

VCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLK (OCIF4)
61
121
HRSCPPGFVVQAGTPERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTKGNAT (OCIF1)

HRSCPPGFVVQAGTCQCAAKLIRIMQSQIVVTV (OCIF4)
121

Fig. 12

1
MNNLLCCALVFLDISIKWTTQETFPPKYLHYDEETSHQLLCOKCPPGTYLKQHCTAKWKT (OCIF1)

MNKLLCCALVFLDISIKWTTQETFPPKYLHYDEETSHQLLCOKCPPGTYLKQHCTAKWKT (OCIF5)
1
61
VCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLK (OCIF1)

VCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLK (OCIF5)
61
121
HRSCPPGFVVQAGTPERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTKGNAT (OCIF1)

HRSCPPGFVVQAGCRRRPKPQICI (OCIF5)
121

Fig. 13

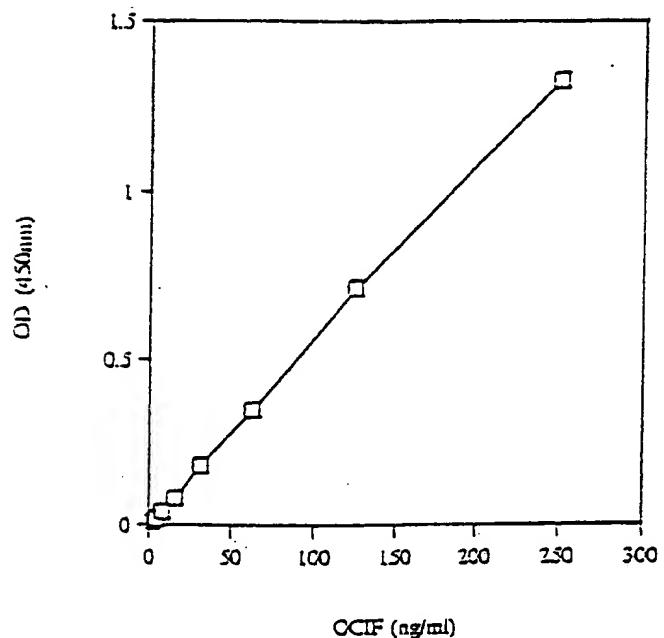


Fig. 14

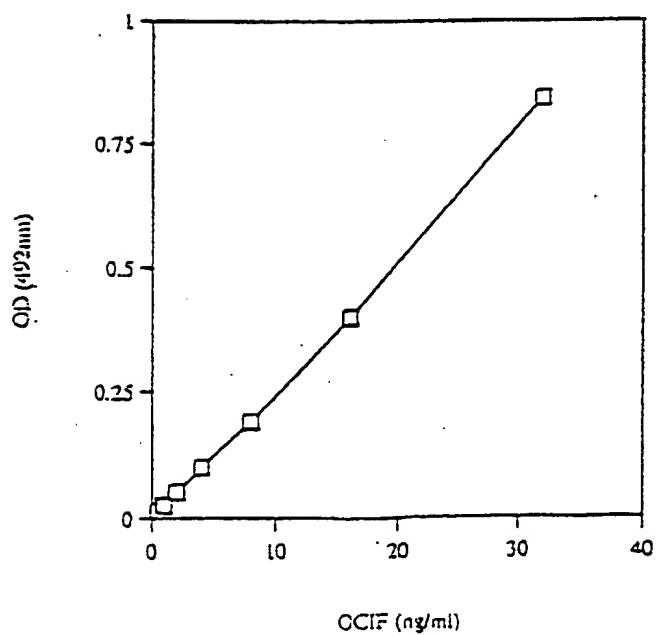
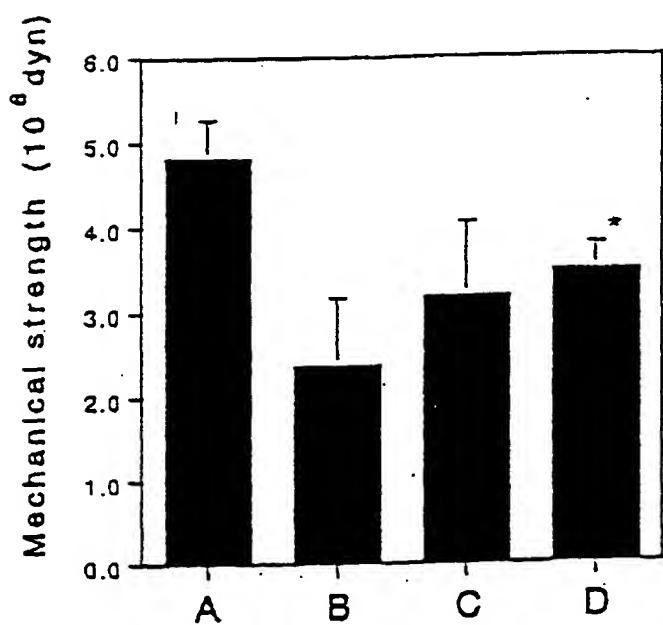


Fig. 15



A : Normal rat

B : Denervated rat+Vehicle

C : Denervated rat+OCIF $10\mu\text{g}/\text{kg}/\text{day}$

C : Denervated rat+OCIF $100\mu\text{g}/\text{kg}/\text{day}$

INTERNATIONAL SEARCH REPORT		International application No. PCT/JP96/00374									
A. CLASSIFICATION OF SUBJECT MATTER Int. Cl ⁶ C07K14/52, C07K16/24, C12N15/19, C12N15/06, C12N5/08, C12N5/10, C12N5/20, C12P21/02, C12P21/08, G01N33/577 According to International Patent Classification (IPC) or to both national classification and IPC											
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) Int. Cl ⁶ C07K14/52, C07K16/24, C12N15/19, C12N15/06, C12N5/08, C12N5/10, C12N5/20, C12P21/02, C12P21/08, G01N33/577											
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched											
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) BIOSIS PREVIEWS, CAS ONLINE, WPI, WPI/L											
C. DOCUMENTS CONSIDERED TO BE RELEVANT <table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="text-align: left; padding: 2px;">Category*</th> <th style="text-align: left; padding: 2px;">Citation of document, with indication, where appropriate, of the relevant passages</th> <th style="text-align: left; padding: 2px;">Relevant to claim No.</th> </tr> </thead> <tbody> <tr> <td style="padding: 2px;">A</td> <td style="padding: 2px;">Fawthrop, F.W. et al. "The effect of transforming growth factor beta on the plasminogen activator activity of normal human osteoblast-like cells and a human osteosarcoma cell line MG-63", J. Bone. Miner. Res. (1992) Vol. 7, No. 12, p. 1363-1371</td> <td style="padding: 2px;">1 - 96</td> </tr> <tr> <td style="padding: 2px;">A</td> <td style="padding: 2px;">Fenton, A.J. et al. "Long-term culture of disaggregated rat osteoclasts inhibition of bone resorption and reduction of osteoclast-like cell number by calcitonin and PTHrP107-139", J. Cell Physiol. (1993) Vol. 155, No. 1, p. 1-7</td> <td style="padding: 2px;">1 - 96</td> </tr> </tbody> </table>			Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.	A	Fawthrop, F.W. et al. "The effect of transforming growth factor beta on the plasminogen activator activity of normal human osteoblast-like cells and a human osteosarcoma cell line MG-63", J. Bone. Miner. Res. (1992) Vol. 7, No. 12, p. 1363-1371	1 - 96	A	Fenton, A.J. et al. "Long-term culture of disaggregated rat osteoclasts inhibition of bone resorption and reduction of osteoclast-like cell number by calcitonin and PTHrP107-139", J. Cell Physiol. (1993) Vol. 155, No. 1, p. 1-7	1 - 96
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A	Fawthrop, F.W. et al. "The effect of transforming growth factor beta on the plasminogen activator activity of normal human osteoblast-like cells and a human osteosarcoma cell line MG-63", J. Bone. Miner. Res. (1992) Vol. 7, No. 12, p. 1363-1371	1 - 96									
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Date of the actual completion of the international search May 14, 1996 (14. 05. 96)	Date of mailing of the international search report May 28, 1996 (28. 05. 96)										
Name and mailing address of the ISA/ Japanese Patent Office Facsimile No.	Authorized officer Telephone No.										